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                                    GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          August 19, 2003, 15:40:25 ; Search time 4747 Seconds
                                                (without alignments)
                                                5225.460 Million cell updates/sec

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Searched:        32997241 seqs, 1638392548 residues

Total number of hits satisfying chosen parameters:        65994482

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	223	5.7	2310	38111	A	US-09-494-297-1	Sequence 38111, A
4	205	5.2	3465	16	US-10-282-122A-38111	Sequence 2717, Ap
5	205	5.2	3465	16	US-09-134-000C-2717	Sequence 2717, Ap
6	205	5.2	3465	53	US-10-434-665-2717	Sequence 2717, Ap
7	196	5.0	15614	15	US-09-070-927-45	Sequence 45, Appl
8	196	5.0	15614	15	US-09-070-927A-45	Sequence 45, Appl
9	192	4.9	7971	58	US-60-045-649-1048	Sequence 1048, Ap
10	192	4.9	8040	58	US-60-046-653-1042	Sequence 1042, Ap
11	192	4.9	11907	60	US-60-068-217-919	Sequence 919, App
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13	182	4.7	2187	52	US-10-417-884-864	Sequence 864, App
14	180	4.6	2127	26	US-09-600-720-17	Sequence 17, Appl
15	180	4.6	2127	49	US-10-269-017-17	Sequence 17, Appl
16	180	4.6	18768	59	US-60-068-186-748	Sequence 748, App
17	180	4.6	18786	59	US-60-050-444-744	Sequence 744, App
18	178	4.5	2694	21	US-60-445-096A-2	Sequence 2, Appli
19	178	4.5	7650	21	US-10-445-096A-1	Sequence 1, Appli
20	177	4.5	2721	21	US-10-282-122A-26784	Sequence 26784, A
21	177	4.5	49617	25	US-09-596-002-28	Sequence 28, Appl
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23	176	4.5	2718	21	US-09-445-096A-69	Sequence 69, Appl
24	174	4.4	2670	49	US-10-282-122A-20971	Sequence 2097, A
25	171.5	4.3	19992	29	US-09-663-779-1383	Sequence 1383, Ap
26	169.5	4.3	14346	16	US-60-063-139-1368	Sequence 1368, Ap
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35	161	4.1	4359	48	US-10-206-576-401	Sequence 401, App
36	161	4.1	12445	15	US-09-070-927-242	Sequence 242, App
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; APPLICANT: PODBIELSKI, ANDREAS
; TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
; FILE REFERENCE: P06628US0/BAS
; CURRENT APPLICATION NUMBER: US-09/494,297
; CURRENT FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 2274

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; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-494-297-1

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Best Local Similarity:	100.00%
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DB:	

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US-09-494-297-2 (1-757) x US-09-494-297-1 (1-2274)

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Db  1381 CGTGACACTCTTTAAATATACTGTGAAACCAAGAGAATACCACTCCATATGTCAGGT 1440

Qy   481 HisIleLeuLysSerValIleGluGlyLysGlyTyrArgGlyLysSerGlyTyrHisGlyTyrAspMetAsnAsp 500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CATATCAAAAAGTAATTGAGAAAGGGTTACAGGGAAAAAGGCAAAGCTATTGGGATTATGAGTATAGT 1500

Qy   501 GlyLeuThrGluThrGlnLeuGlnArgGluAlaAlaThrGlnLeuLeuAlaIleGluTyrIleTyrrPheThrArgAsp 520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 GGTCTAACTGAGACACAATTGCCTGCGCCTACTCAGTTAGCAATAATATATTTCACTCGAT 1560

Qy   521 SerAlaGluLeuAspLysLysSerAspLysLysSerAspProTyrHisGlyTyrAspMetAsnAsp 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 AGTGCTGAATTAGATAAGATAAAGACTAATCCATAGGTTTTTGGACACATGAATGAT 1620

Qy   541 SerThrLeuAlaValAlaLysLysIleLeuGluValAlaGlnAspSerAsnProProGln 560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 AGTACTTTAGCAGTTGCTAAAAAATCCTTCGAGAATAGGATAGTAATCGTCCCACAG 1680

Qy   561 LeuThrArgAspPhePheIleGluProAsnAsnAsnLysSerTyrGlnSerIleGlyThr 580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CTAACTAGACCTTGATTCTTTATTCCGGAATAACAATAAATATCAATTCTTATTGGAACT 1740

Qy   581 GlnTrpHisSerProGlyAspProLeuValAspLeuGluArgMetGluAspLysLysGluValIle 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CACTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAAAAGAAGTTATA 1800

Qy   601 ProValThrArgHisAsnLeuThrLeuArgLysSerThrValThrGlyGluValAlaGlyLysAspArgThr 620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CCTGTAACTCTAAATTTAACATTGAGAAAACGGTGACTGGTTAGCTGGTGACAGAACT 1860

Qy   621 LysAspPheHisPheGluIleLeuLeuLysAsnAsnLysSerGlnLeuLeuSerGlnThr 640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AAAGATTTCCATTTTGAAATTAAAGCAAGAAATAATAAGCAAGAATTGCTTTCTCAAACT 1920

Qy   641 ValLysThrHisAspLysThrAsnLeuGluPheLeuLysAspGlyLysAlaThrLysIleLeuAsnLeuLys 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GTTAAAACAGATAAAAACAAACCCTCGAATTTAAAGATGGTAAAGCAACCATTAATTTAAAA 1980


Qy   661 HisGlyGluSerLeuThrLeuGlnLeuGlyLeuProGluGlyTyrSerTyrLeuValLysGlu 680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGTTATTCTTACCTTGTCAAAGAA 2040

Qy   681 ThrAspSerGluGluGlyTyrLysValLysValLysAsnSerGlnGluValAlaAsnAlaThrVal 700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 ACAGATTCTGAAGGCTATAAGGTTAAAGTTAAAGTAGCCAAGAAGTAGCAAAATGCTACAGTT 2100

Qy   701 SerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProVal 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TCAAAAACAGGAATAACAAGTGATGAGACACTTGCTTTTGAAAATAATAAAGAGCCTGTT 2160

Qy   721 ValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIleIleAlaGly 740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GTTCCTACAGGAGTTGATCAAAAGATCAATGGCTATCTAGCTTTGATAGTTATCGGT 2220

Qy   741 IleSerLeuGlyIleIleTrpGlyIleHisThrIleArgIleArgLysHisAsp 757
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 ATCAGTTTGGGGATCTGGGAATTCACACGATAAGGAATAAGAAACATGAC 2271
```

RESULT 2
US-09-494-297-3
Sequence 3, Application US/09494297

GENERAL INFORMATION:
APPLICANT: PODBIELSKI, ANDREAS
TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
FILE REFERENCE: P0662BUS0/BAS
CURRENT APPLICATION NUMBER: US/09/494,297
CURRENT FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2229
TYPE: DNA
ORGANISM: Streptococcus pyogenes
US-09-494-297-3

Alignment Scores:
Pred. No.:
Score: 3.69e-161   Length: 2229
Percent Similarity: 1965.50   Matches: 409
Best Local Similarity: 70.00%   Conservative: 116
Query Match: 54.53%   Mismatches: 192
DB: 49.82%   Indels: 34
                           21   Gaps: 16

US-09-494-297-2 (1-757) x US-09-494-297-3 (1-2229)

```
Qy    20 SerLysAsnSerLysArg------PheThrValThrLeuValGlyValPheLeuMetIle 37
         |||::::||||||     |||:::||||:::||:::||
Db    31 AGCGCTAACAACAAACGACGACAAATTCAAGATTACGGATTACTGAAAGTATTTTGACGTTT 90

Qy    38 PheAlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSerSer 57
         :::                       :::
Db    91 GTAGCTCTGATAGGAATAGTAAGGGTTTTCATCAGAGCGGTTCGGAGCTGAAGAACAATCA 150

Qy    58 ThrProAsnAlaIleAsnProAspSerSerGluThrArgArgTyrArgTyrGlySer 77
         |||      |||:::|||   ::::||
Db   151 ACAACAAAGCTCAATTCAAGATTATCCGTGGTATGGCTATGAGATTCT 204

Qy    78 TyrValArgGlyHisProTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsn 97
         |||  :::||||::||||||||::::
Db   205 TATCCTAAAGGCTACCCAGACTATAGTCCGTTAAAGACTTACCAATAATTAAAAGTAAAT 264

Qy    98 LeuGluGlySerArgSerTyrGlnValThrCysPheAsnLeuLysLysAlaPheProLeu 117
         |||||::|||::||||||::
Db   265 TTAGAGGGAAGTAAGGAATATCAAGCATACACTGCTTTAATTTAACAAACATTTTCATCC 324

Qy   118 GlySerAspSerSerValLysTrpTyrLysLysHisAspGlyIleSerThrLysPhe 137
         |||:::|||||||::::||||
Db   325 AAGTCAGATAGTGTTAGATCACAAATGGTATAAAAAACTTGAAGGAACTAATGAAACTTT 384

Qy   138 GluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAla 157
         |||      |||  :::|||   :::
Db       GTTAAAACAGATAAAAACAAACCCTCGAATTTAAAGATGGTAAAGCAACCATTAATTTAAAA 1980
```

```
Db   385 ATCAAGTTAGCAGATAAACCAAGAGAATAGAAGACGGACAGTTACAACAAAATATATTGAGG 444
                      ||||||||  ||||:::::    ||:::|  |||  | ||||:   |:||:||||
Qy   515 IleThrTyrPheThrAspSerArgAlaGlyLeuAspLysLeu---------------Lys 530
Db  1486 ACCTATTATTTTACAGACAGTTGCTGACTTTAAAAAACCTTTAAAAAACAATGGGAAA 1545

Qy   158 ValMetThrTyrAsnGlyHisProGlnAsnGlyIleMetGluGlyLeuProLeu 177
Db   445 AATTCTCTTATTAATGGATAATCGTAATTAATCGTAATGGGATAATCCTTCTA 504

Qy   178 AsnAlaIleArgValThrGlnGluAlaValIleProTyrTyrSerAspAsnAlaProIleSer 197
Db   505 AACGCTATTTTAGTGCAACTCAAAAATGCTATTGG---TATACTGATTCAGCTCAAATT--- 558

Qy   198 AsnProAspGluSerPheLysArgGluSerAsnLeuValSerThrSerGlnLeu 217
Db   559 AATCCGGATGAAAGTTTTAAAGAAGCTTTAAAACAGAAGGTCGAAGTAATGTGTTAT 618

Qy   218 SerLeuMetArgGlnAlaLeuLeuLysLysGlnLeuIleAspProAsnLeuAlaThrLysMetPro 237
Db   619 GGCTTAATGCGACAAGCTTTAAATGAAGAACTTATTGATCCAAATTTAGGGCAAACAATTCG 678

Qy   238 LysGlnValProAspAlaSerPheGlnLeuSerGluAlaThrLysMetPro 257
Db   679 AATAAAACCATCAGGTTATCGGTTTAAAATGTATTGAATCTCATGAT 726

Qy   258 TyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyTyrLeuValProThrLysProProThr 277
Db   727 ------AAGCCTTCCAAAAATCTTTGAGTCGTGAGTATGTTCCGGATACTCCCCAAAA 780

Qy   278 ProGlyAspProPoMetProProAsnGlnThrThrSerValLeuIleArgLys 297
Db   781 CCAGGAGAAGAG------CCTCCGGCTAAAACTGAAAAACATCAGTCATTATCAGAAAA 834

Qy   298 TyrAlaIleGlyTyrSerLysLeuLeuGluGlyLyAlaThrLeuGlnLeuThrGlyAsp 317
Db   835 TATGCGCAAGGTGAC---TCTAAACTTCTAGAGGCGGCAACCTTAAAGCTTTCTCAAATT 891

Qy   318 AsnValAlaSerPheGlnAlaAargValPheSerSerAsnAsproIleGlyGlyLeuArgIleGlu 337
Db   892 GAAGGAAGTGGTTTCAAGAAAAAAGCTTTCAAAGTAAATAGTTTAGGAGAAAACTGTCGAA 951

Qy   338 LeuSerAspGlyThrThrPheLeuThrGluLeuAsnSerProAlaGlyThrTyrSerIleAla 357
Db   952 TTACCAAATGGGACTTATACCTTAACAGAAAACATCAGTCCAGATATAAAATTGCG 1011

Qy   358 GluProIleThrPheLysValGluAlaGlyLyLyAlaThrArgIleThrIle---IleAspGlyLys 376
Db  1012 GAGCCGATTAAGTTTGAGGAGAGGAATAAAAGTGTTTAACGTCCAAAAGATGGTTCT 1071

Qy   377 GlnIleGluAsnProAsnLysGluIleValGlLProTyrSerValGluAlaLaTyrAsnAsp 396
Db  1072 CAAGTGGAAAATCCAAACAAAGAAGAGTAGCAGAGCCATACTCAGTGGAAGCCTATAATGAC 1131

Qy   397 PheGluGluPheSerValLeuThr---ThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
Db  1132 TTTGAGGAGTTATGGTAGAAGTACTCTCGGGTTTACTCCAACGGAAAAATTCTATTACGTTCA 1191

Qy   416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435
Db  1192 AATAAGGATAAAAGTTCACAAGTGTCTACTGCTTCAAATCGTTACTCACCACCT 1251

Qy   436 AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThr---GlyGluValLys 454
Db  1252 GACTCATATGATGGTGGTGAGACTATAAAATCCAGATAACTAGTACGATAAGAGTCAAG 1311

Qy   455 TyrThrHisIleAlaGlyArgGlyAspLeuPheLysTyrThrValLysProArgAspThrAsp 474
Db  1312 TACACACATACGGCAGGTAGTGACTTGTTTAAAATATGGCGTAAGACCGAGAGATACAAAT 1371

Qy   475 ProAspThrPheLeuLysHisIleLysLysGlyTyrArgGluLysGly 494
Db  1372 CCAGAAACACTTCTTAAAGCACATTAAAAAAAGGTAATGAAAAAGTTACAGAAAAAGGT 1431

Qy   495 GlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgGlnLeuLeuAla 514
Db  1432 GATAGC-----TATAATGGATTAACAGAAAACACAGTTCGCGCGGCTACTCAGCTTGCT 1485
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```
Qy   530 Lys
Qy   515 IleThrTyrPheThrAspSerArgAlaGlyLeuAspLysLeu---------------Lys 530
Db  1486 ACCTATTATTTTACAGACAGTTGCTGACTTTAAAAAACCTTTAAAAAACAATGGGAAA 1545

Qy   531 AspThrTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaAlaLysIleLeuVal 550
Db  1546 GGTTACCATGGAATTGAATCTACTTTGGCAGTTGCAGCAAAACTTAGCGCTGTCACAAAAGAATTAATT 1605

Qy   551 GluTyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePhePheIleProAsn 570
Db  1606 ACTTATGCTCAAGATTCAAATCCGCCCCCAACTAACAAAATCTTAGATCTTGACTTTTTCTTTATTCCTAAT 1665

Qy   571 AsnAsnLysTyrGlnSerIleLeuIleGlyTyrGlnIleHisProGlnLeuAspSerMetPro 590
Db  1666 AATAGCAAAAGCAACCAAATCCTTAATTAGGGGACAGAATTCACAGTTTGACAGTGAA 1725

Qy   591 IleLeuArgMetGluValIleProValSerLysProLysSerGlyAspLys 609
Db  1726 ATTCGTATGGAAGTAATAAAACCAAGAGTTAATCCAAAATCAGGTTTGACAGTTGAAA 1785

Qy   610 LysThrValThrGlyLeuValGlyAspArgThrLysAspSerPheHisSerPheGluIleGluLeu 629
Db  1786 AAAACAGTAGTCGGGTGAGTTGGGAGATAAAACTAAAAGGCTTCCAATTGACATTGAACTTGAGTTG 1845

Qy   630 LysGlnAsnAsnLysGlnLeuLeuLeuSerGlnThrValLysThrGlyIleLeuThrSerAspGlu 649
Db  1846 AAAGATAAAAACTGGACACAGCCTATTGTTAACACTCTAAAAACTAATAATCAAGATTAGTA 1905

Qy   650 PheLysAspGlyLysGlyAlaThrIleAspAsnLeuLysLysHisGlySerLeuThrLeuGlnGly 669
Db  1906 GCTAAAGATGGGAAAGATATTCATTTAAATCTAAAACCATGGTGACACCATAAGAATAGAAGGA 1965

Qy   670 LeuProGluGlyGlyTyrSerTyrLeuValGlyGluSerGluGluGlyGlyTyrLysLysValLys 689
Db  1966 TTACCGGACGGGATATTCTTATACTGTCGAAAGCTGAAAGCTAAGGATATATAGTAACC 2025

Qy   690 ValAlaAsnSerGlnGluValAlaLeuAlaAsnAlaThrValSerLysThrGlyIleLeuThrAspGlu 709
Db  2026 GTTGATAACAAAAGTTAGTCAAGAAGCCAGTAGAGGTCAGTAGGTAGGTATAAACAGAGACAAA 2085

Qy   710 ThrLeuAlaPheGluAsnAsnLysGlnProValValValProThrGlyValAspLysLysIle 729
Db  2086 AAAGTCACTTTTGAACAGAAATCTTGTCCACCAACTGGTTT-GACAACAGAAGG 2144

Qy   730 AsnGlyTyrLeuAlaLeuIleValValIleAla----------GlyIleSerLeuGlyIle 745
Db  2145 ---GGCTATCTATCTTTGGGTGTTGTTATTACTTGTTCCACTTGGGTTGTTTGGCTATT 2201

Qy   746 TrpGlyIleHisThrIleArgIleArgLys 755
Db  2202 TGG--------TCGTAAAGGGTAAAAAAA 2222
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; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38111
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-38111

Alignment Scores:
Pred. No.:
Score:                 1.31e-08
Percent Similarity:    223.00
Best Local Similarity: 35.23%
Query Match:           21.06%
DB:                    5.65%
                       49

US-09-494-297-2 (1-757) x US-10-282-122A-38111 (1-2310)

                       Length:          2310
                       Matches:         159
                       Conservative:    107
                       Mismatches:      259
                       Indels:          230
                       Gaps:            40
```

```
Qy     21  LysAsnSerLysArg---------PheThrValThrLeuValGlyValPheLeuMetIlePhe    38
               ||||||||||                      ::: |||||||||| ::
Db     10  AAAAATAAGCTATAAAGTTAAGCTTCCTGTTATCCCTAACAGGA------------TTTATTTTTA  60

Qy     39  AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSerSerThr       58
               ||:||                 |||          :::          |||
Db     61  GGTTTATTATTGGTTTTTATAGGATTGGTTTGTCCGGAGTA----TCAGTAGGACATGCGGAAACA  117

Qy     59  ProAsnAlaIleAsnProAspSerSerSerGlyGlyLysSerGlyTyrArg--------------  Trp  72
               |||             :::  |||  ::                 ||| 
Db    118  AGAAATGGACGAAACAACAAGGAGCGTTTGAAATCAAGACAAAATAAAAGTCAAGAAGAA       177

Qy     73  TyrGlyTyrGlyGluSerTyrValArgGlyHisProThrTyrTyrLysGlnPheArgValAlaHis  92
               |||              |||                :::          ||| 
Db    178  TATAATTATGA------------------------GTTTATGATAACAGAAACATACTTCAG       216

Qy     93  AspLeuArgValAsnLeuGluGlySerArg---------------SerTyrGlnVal         106
               |||                                      :::|||||||
Db    217  GATGGGGAACAATAAACTTGAAATAAAAAGAGTTGATGGGGACAGGTAAAACTTATCAAGGT      276

Qy    107  TyrCysPheAsnLeuLysLysAlaLeuProLeuGlySerAspSerSerValLysLysTrp       126
               ||||||              |||          ::: ||||||||
Db    277  TTTTGCTTTCAGTTAACGAAAAAATTTCCACTGCTCAGGGTGTAAGT--AAAAAGCTG          333

Qy    127  TyrLysLysHisAspGlyIleSerThrLysPheGluAsp------------------------   139
               :::||||||              ::: |||
Db    334  TATAAAAAA-----------TTGATGTAGTAGTGATGAGAAAACTAAGCAATATGCCTCT       384

Qy    140  ---TyrAlaMetSerProArg---IleThrGlyAspGluLeuAsnGlnLysLeuArgAla       157
               ::: |||                :::||||||:::::
Db    385  AAAATAATACAGATAATAGGAGAGAGAGATACTAGTTGGTTTAATCTTTAAAAAGCAAATTTGCTAAG  444

Qy    158  ValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeu       177
               ||||::                ||||||
Db    445  GTTCTGACAGAAGGTTACCCACTAACAAAAAGTGATTGGTTAAATGGATTGACTGAAAAC       504
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```
Qy    178  AsnAlaIleArgValThrGlnGluAlaValThrTrpTyrTyrSerAspAsnAlaProIleSer     197
               |||||||||||||||        :::    ||| ::::
Db    505  GAAAAAAATAGAAGTAACCCAGGATGCAATTTGGTATTTTACAGAAAGGACAGTTCCGGCT      564

Qy    198  AsnProAspGluSerPheLysArgGluSerGluAsnLeuValSerThrSerGlnLeu          217
               |||          ::: |||                                      |||
Db    565  ------GATAGAAGTTATACGAATCGCAACGTAAATAGT------------------------   597

Qy    218  SerLeuMetArgGlnAlaLeuLysGlnLeuIleLeuAspProAsnLeuAlaThrLysMetPro     237
               |||::::::                 |||||||||||||||||||
Db    598  CAAAAAATGAAAGAAGTGTATCAAGAAAGCTAAATTGAT----ACAACAGATATAGAT         648

Qy    238  LysGlnValProAspProAspPheGlnLeuSerIlePheGluSerGlyLeuAspLysPheLys     257
               :::|||        |||          :::          ::|||
Db    649  AAATAT---------GAAGAGTACAAATTTGATTTATTTGTGCCACAAGAT-----------   690

Qy    258  TyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyLysGlyLeuValLeuProThrLysProThr    277
               :::::                                                 |||
Db    691  ------ACAAACTTTACAGCGCAGTAATTAGT----GTAGAGCCTGTTATCGAAAGCCTT      738

Qy    278  ProGlyAspProMetProProAsnGlnProGlnThrThrSerValLeuIle-------------    295
               |||                    |||:::          ||| :::::
Db    739  CCTTGGACATCGTTGAAGCCAATAGCCCAGAAGGATATCACTGCAAAAAAATCTGGGTA         798

Qy    296  ---ArgLeuTyrAlaIleGlyAspTyrSerLysLeuLeuAsnSerProTyrAlaIleGlyAlaThr  311
               |||          ::                          :::||||||:::||||||
Db    799  GATGCACCTAAAAGAAAAAACCAATTATT----TATTTTAAGCTATATAGA-               843

Qy    312  LeuGlnLeuThrGlyLysAspAsnSerPheGlnAlaArgValPheSerSerAsnAsp          331
               |||||||                |||      :::
Db    844  --CAGCTGCCCTGGAGAAAAG---------------------------------------       861

Qy    332  IleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrLeuGluAsnSerPro       351
               ||                          ||| ::
Db    862  -----------------GAAGTAGCAGTGGGATGACGCCTGAGCTAAAAACAGATAAAATAGTGAA  906

Qy    352  AlaGlyTyrSerIleAlaGluIleThrPheLysVal----------GluAlaGlyLys         368
               ||||::::::          ||| ::
Db    907  GGTCAACAAGAAAATTCAGTAACTTGGACAAAATCAACTTGTTACAGATGAAAAAGGAATG  966

Qy    369  ValTyrThrIleIleAspGlyLysGlnIleGlnLeuAsnProAsnLysGlyValGluGluPro    388
               ||| |||                ::|||
Db    967  GCTTTAT---ATTTATTCTGTTAAAGAAGTAGAATAAA--AATGCCAGTTACTTGAGCCA        1020

Qy    389  TyrSerValGlyAlaLysTyrAsnAspPhe----GluGluPheSerValLeuThrThrGlnAsn    407
               |||                               :::
Db   1021  -------------------AAAGATTATATCAGAAGAAGAAAGGGACTTACAGTTACTAAT      1062

Qy    408  TyrAlaLysPheThrTyrAlaLysAsnGlySerSerGlnValValTyrCysPhe          427
               |||                ||| ::                        |||
Db   1063  ---ACTTATGTAAAGCCAACTAGTGGGCACTATGATAATAGAAGTGACACATTT          1110

Qy    428  --AsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrPro        446
               :::          |||                                ||| 
Db   1111  GGAAATGGACATATATGGATAATTACAGAGAGATACT-----------ACACA            1149

Qy    447  AspPheThrPheGlyGluValLysTyrThrHisIleIleAlaGlyArgAspLeuPheLysTyr    466
               ||| ::::::          ::: |||          ||| |||
Db   1150  GATATTGTTTTCAGGTGAAAAACCAAATGAAGCAAATAGAGGGAGAAGAT---------         1197

Qy    467  ThrValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIle       486
               |||||||||              |||
Db   1198  ---AGTAAGCCTATTGATGAA--------------------------------------       1215

Qy    487  GluLysGlyTyrArgGlyLeuThrGlnIleAlaIleGluThrTyrSerGlyLeuThrGlnThrGln 506
               |||          :::          ||| |||
Db   1216  ---------------------------------------GTAACGGAAAATAAT            1230

Qy    507  LeuArgAlaAlaThrGlnLeuLeuAlaIlePheTyrTyrPheThrAspSerAlaGluLeuAspLys 526
               ||||||
Db   1230  ------------------------------------------------------        1230
```

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Qy  527   AspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaAla  546
Db  1230   ...                                                              1230

Qy  547   LysIleLeuValGluTyrAlaGlnAspSerAsnProGlnLeuThrAspLeuAspPhe        566
Db  1231   TTAATTGAATTTGGTAAAACACGATGCCAGGTGAAGAAGATGGC---------           1275

Qy  567   PheIleProAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAsp        586
Db  1276   ---ACAAATTCTAATAAGTATGAA--                                      1296

Qy  587   LeuValAspIleIleArgMetGluAspLysLysGluValIleLeuProValThrHisAsnLeu  606
Db  1297   ----GAAGTCGAAGACTCACGCCCAGTT--                                  1329

Qy  607   ThrLeuArgGlyThrValThrGlyLeuAlaGlyArgThrLysAspPheHisPheGlu        626
Db  1330   TCAGGTTTATCAAGTGAGCAAGGTCAGTCCGGTGATATGACAAATTGAAGAAGATGTGCT    1389

Qy  627   IleGluLeuLysAsnAsnLysGlnGluLeuSerGlnThrValLysThrArgAspLysThr     646
Db  1390   ACCCATATTAAATTCTCAAAACGTGATATTGACGGCAAAGAGTTAGCTGGTGCAACTATG    1449

Qy  647   AsnLeuGluPheLysAspGlyLysAlaThrIleAsn---LeuLysHisLysGlyGluSer     664
Db  1450   GAGTTGCGTGCATTCATCTGGTAAA--ACTATTAGTACATGGATTAACGACAAAGT        1506

Qy  665   LeuThrLeuGlnGlyLeuProGlyLeuGlyTyrSerTyrLeuValLysGluThrArgSerGlu  684
Db  1507   AAAGAATTTCTACCTGATGCCAGGAAAAATTATACATTT--GTCGAAACCGCAGCACCAGAC  1563

Qy  685   GlyThrTyrLysVal---LysValAsnSerGlnGluValAlaAlaAsnAla             698
Db  1564   GGTTATGAGGTAGCAACTGCTATTACCTTACAGTTAATGAGCAA----GGTCAGGTT      1617

Qy  699   ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysSerGlu  718
Db  1618   ACTGTAAAATGCAAAGCACAACTAAAAGGTGACGCTCATATTGTCAGGTTGAIGCTTACAAG  1677

Qy  719   ProValProThrGly---ValAspGlnLysIle                              729
Db  1678   CCAACTAAGGGTTCAGGTGTCAGGTTGAITTGAIATATTGAAGAAAAGCTT            1722
```

RESULT 4
US-09-134-000-2717
Sequence 2717, Application US/09134000A

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-005

CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 6810

SEQ ID NO 2717
LENGTH: 3465
TYPE: DNA
ORGANISM: Enterococcus faecalis

US-09-134-000-2717
SEQ ID NO 2717
LENGTH: 3465

```
Length:                 3465
Matches:                170
Conservative:           85
Mismatches:             236
Indels:                 231
Gaps:                   43
```

Alignment Scores:

```
Pred. No.:
Score:                  8.26e-07
Score.                  205.00
Percent Similarity:     35.37%
Percent Identity:       23.58%
Best Local Similarity:  5.20%
Query Match:            16
DB:
```

US-09-494-297-2 (1-757) x US-09-134-000-2717 (1-3465)

```
Qy  88   PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer----------ArgSerTyrGln  105
```

```
Db  1781  TTCAGGTTCAAACATTA-CCAGAAGTGTCGGCTAACAGGGCGTCGCTACAATTAATAGTAGTGAG  1839

Qy  106  ValThrCysPheAsnLeuLysLysAlaLysPheProLeuGlySerSerSerValLysLys        125
Db  1840  ATTTAT--                                                          1872

Qy  126  TrpTyrLysLysHisAspGlyIleIleSerThrLysSerGluAsp-------               139
Db  1873  CATTATCAAGTACGT-----ATTTCAAACACAGTCAGAAAAACTTCAAACCTGATTTTTGG     1926

Qy  140  TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet       159
Db  1927  TATCAAATGAATAGGTCGGACAACGTTCAGCCATTAGCCACGGCCCCTGAAAAAGTTGAT      1986

Qy  160  TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla       179
Db  1987  TTT------GGGGTTCCTTGCGGAAAAGCCACT--GGC                            2016

Qy  180  IleGluArgValThrGlnIleuAlaValThrTyrTyrSerAspAsnAlaProIleSerAsnPro   199
Db  2017  GTGAAGTTAAACGTGAAAAAAATTCTGGGAAGAGTAATGATCAAGACCCGACAAGTCGGCCA    2076

Qy  200  AspGluSerPheLysArgGluSerGluAsnLeuValSerThrSer---                  215
Db  2077  GATAAAGTGATTTTATGAAAATTAGTAGAAGCAGAAGTAACTGACACGCCAACTGGCAAACT    2136

Qy  216  ------GlnLeuSerLeuMetArgGlnAlaAsnGlyLeuLeuIleuAspProAsnLeu         232
Db  2137  GGGTATATTAAATTATCAAAAAACCAGAAAATGATCCAGACAATAGTTGGGACGGCAAAAT     2196

Qy  233  AlaThrLysMetProLysGlyValProAspProAspPheGln---LeuSerIlePheGlu       250
Db  2197  GTAACCCAACTTTTCCAAAACGCGGATGAAAGCTATCAAGAAGCTTCTTGTGGGCTTCCCAA    2256

Qy  251  SerGluAspLysGlyLysAspLysLysTyrAsnLysGlyGlyTyrGlnAsnLeuLeuSerGlyIleGlyLeu  270
Db  2257  TACAACAATCAAGGACAAGCTTTCAAT-----TATCAAACAACCCGTGAATTAGCA--       2307

Qy  271  ValProThrLysProProThrProGlyIleAspProProGlnMetProProAsnGlnPheGlnThr--  290
Db  2308  GTTCCTCGGTTACAGTCAGCAGAAAAATGCACGATACTACTGGAAAAACACGAGCAAGTC     2367

Qy  291  ThrSerVal----LeuIleArgLysTyrTyrAlaIleGlyIleAspSerTyrSerLysLysLeu   307
Db  2368  AAGCCATTAGATTTAAAAGTAATCAAAAATTCTTCCTCAGGTGAG-----AAAAACTTA       2421

Qy  308  GluGlyAlaThrLeuGlnLeuThrHrGlyAspAspAsnValAsnSerPheGlnAlaArgValPhe   327
Db  2422  GTGGGAGCCGCGGTCTTTGAATTCGAGTCGGTAAAAAATGTT-----CAAACAACATTAGTG  2472

Qy  328  SerSerAsnAsp----IleGlyGluArgIleGluGluLeuSerAspGly---Thr           342
Db  2473  GACAATAAAGATGGTAGCTATTCCTTGCCAAAAAAGATGTGCGCGGCCTACAAAAAGGGGAACGC  2532

Qy  343  TyrThrLeuThrPheGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe    362
Db  2533  TATACAATTAACTGAGTAAAAGCACCTGCAGGACATGAGTTAGGCAGAGAAAACGACTTGG     2592

Qy  363  LysValGluGluAla---GlyLysValTyrThrIleIleAspSerGlyLysGlnIleGlu      379
Db  2593  CAAAATTGAGGTGAGGTGAGCAAGGCAAAGTA------AGCATCGATGGACAAGAAGTGACC    2646

Qy  380  AsnProAsnLysGluIleValIleGluProTyrSerValGluAlaTyrAsnAspPheGlu      399
Db  2647  ACCACAAAATCAAGTATTT-----CCATTGGAAAATGAA-----AATAAAATTTCTTCT     2694

Qy  400  PheSerVal---LeuThrThrGln---AsnTyrAlaLys                          410
Db  2695  TTGCCAAATCAGAATTAGAAAAAATACACCATGCAAAATGGCAAACACAGTGAACTTAGCAGAG  2754

Qy  411  PheTyrTyrAla---LysAsnLysAsnGlySerSerGlnValValTyrCysPhe           427
```

```
RESULT 5
US-09-134-000C-2717
 Sequence 2717, Application US/09134000C
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2717
;  LENGTH: 3465
;  TYPE: DNA
;  ORGANISM: Enterococcus faecalis
US-09-134-000C-2717
```

Alignment Scores:
```
Pred. No.:              8.26e-07        Length:       3465
Score:                   205.00        Matches:       170
Percent Similarity:      35.37%        Conservative:   85
Best Local Similarity:   23.58%        Mismatches:    236
Query Match:              5.20%        Indels:        231
                             16        Gaps:           43
```

US-09-494-297-2 (1-757) x US-09-134-000C-2717 (1-3465)

```
Qy   88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer------ArgSerTyrGln  105
        |||||                        ||:::||   ||  |||          :::
Db 1781 TTCAGGTTCAAAACATTA-CCAGAAGTGTCGCTTACCAGGCCGCTACAATTAATAGTAGGAG 1839

Qy  106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys  125
        ::                   ||||||:||
Db 1840 ATTTAT--                 TTGGGTAAAGGCGCAAGAAATTCAAATT 1872

Qy  126 TrpTyrLysLysHisAspPGlyIleSerThrLysPheGluAsp-----             139
         |||::                 |||:::
Db 1873 CATTATCAAGTACGT-----ATTCAAACAGAGTCAGAAAACTTCAAACTGATTTTTGG 1926

Qy  140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet  159
         |||                    :::||
Db 1927 TATCAAAATGAAATGGTCGGACAACGTTTCAGCCATTAGCCACGGCCGCCCTGAAAAAGTTGAT 1986

Qy  160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlnGlyLeuGluProLeuAsnAla  179
         |||:::                 |||
Db 1987 TTT--                 GGGGTTCCTTCGGGAAAAGCACCT--GGC 2016

Qy  180 IleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro  199
         ||:::||                |||||::|
Db 2017 GTGAAGTTAACGTGAAAAAATCTGGGAAGAGAGTAGTATGATCAAGAACCGACCAGAAGTCGGCCA 2076

Qy  200 AspGluSerPheLysArgGluSerGluAsnLeuValSerThrSer----------        215
         |||                    ::: :::
Db 2077 GATAATGTGATTATGAAATTAGTAGAAAAGCAAGTAAACTGACACAGCCAACTGGCAAACT 2136

Qy  216 ------GlnLeuSerLeuMetArgGlnAlaLeuLysLysGlnLeuLeuIleAspProAsnLeu  232
              :::||                ||||||
Db 2137 GGGTATATTAAAATTATCAAAAACCAGAAAATGATACCAGCAGCCAATACAGTTGGAGGCGAAAAAT 2196

Qy  233 AlaThrLysMetProLysGlnValProAspAspSerPheGln-----LeuSerIlePheGlu  250
         |||:::||               |||
Db 2197 GTAACCCACACTTTCCAAAAACCGCGGATGAAAGCTATCACAGAAAGTTCTTGGGCTTCCCA 2256

Qy  251 SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu  270
         :::||                  ::::|||
Db 2257 TACAACAATCAAGGACAAGCTTTCAAT------TATCAAACAACCGTGAATTACCA--- 2307

Qy  271 ValProThrLysProProThrProGlyAspProMetProProAsnGlnProGlnThr  290
         ||||||                 |||
Db 2308 ...                                                   2307
```

```
Db 2755 CGCACTTTTGCGTTGCAAAGAAAAATGCTCAAGGAAGTTACCAAACTGTGGCAACTCAA 2814
Qy  428 AsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyGlyLysThrMetThrProAsp  447
        |||
Db 2815 AAAACAGAT                                              2823

Qy  448 PheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThr  467
        ::::|||
Db 2824 --ACTACAGGA--                                          2832

Qy  468 ValLysProArgAspThrAspProAspPheLeuLysHisIleLeuLysSerValIleGlu  487
         |||     :::         |||:::
Db 2833 ------TTGAGCTATTTT--AAAAATTAGTTGAA                     2856

Qy  488 LysGly---TyrArgGluLysGlyGlnAlaIleGluIleTyrSerGlyLeuThrGlyThrGln  506
         ||| |||                |||:::
Db 2857 CCTGGTGAGTATCGA--ATGGTGGACAAATCAGGA                    2892

Qy  507 LeuArgAlaAlaThrGlnLeuAlaIleThrTyrTyrPheThrArgAspSerAlaGlyGluLeuAspLys  526
         |||                    :::         CCA
Db 2893 TTAGGCTACGACACTCCTTGCCTGGAAAATTATGAATTTACT---          2940

Qy  527 AspLysLeuLysAspThrTyrHisGlyPheGlyAspMetAlaAsnAspSerThrLeuAlaLeuAla  546
         |||:::||
Db 2941 ------TATGGGAAA                                        2949

Qy  547 LysIleLeuValAlaGluTyrAlaGln---                         563
         |||:::                 AspSerAsnProProGlnLeuThrThrAsp
Db 2950 ATTCACTATGCAGGCAAAAATATTGAAGAAAAATGCGCCAGAAATGGACA--   2997

Qy  564 LeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHis  583
        :::                     |||:::
Db 2997 ------GTTGATAAA                                        2997

Qy  584 ProGluAspLeuValAspIleIleArgMetGluAspLysLysGlyValIleIleProValThr  603
         ||||||                 |||
Db 2998 ------CTGACA                                           3003

Qy  604 HisAsnLeuThrLeuArgLys---                               620
         |||:::                 ThrValThrGlyLeuAlaGlyIleAspArgThr
Db 3004 CATCAAAATAATTTGAAACCTTTGACTTAACAGTTCATAAAAAAGGCCGATAATCAGACG 3063

Qy  621 LysAspPheHisPheGluIleGluLeuGluLysAsnAsnLysGlnGluLeuSerGlnThr  640
         |||                    :::
Db 3064 ------CCACTTAAAGAGACGCGAAAATTCCGTTTTAACAGGA---         3096

Qy  641 ValLysThrAspLysThrAsnLeuGluPhe---                      656
         |||                    :::||            LysAspGlyLysGluAsnGlyTyrPhe
Db 3097 ------CCAGATACGGATATTGAATTACCAAAAGATGGCAAAGAAAACGGATACTTTT 3147

Qy  657 ---IleAsnLeuLysHisGlyGlu---                            673
            |||:::                ||||||   SerLeuThrGluLysGlnGlyLysAsnSerSerAsnArgLysThrPheThrProGluGly
Db 3148 GTTTTTGAAAACTTAAAAACCAGGGAAAAATAGTTCTAACAGAAAAACCTTTACGCCGAGAGGA 3207

Qy  674 TyrSerTyrTyrLeuValLysGluThrAsp------                   690
         |||                    :::         SerGlyGlyTyrLysLysGlyValLeuThrThrSer
Db 3208 TATCAGGGGTTAAAAGAACCAATACGAATTAAATTGGTTAGAAGATGGTTCACTCACGATA 3267

Qy  691 AsnSerGlnGlyValAlaLeuAsnAlaThrValSer---               707
         |||:::                  ||||||            LysThrGlyIleLeuThrSer
Db 3268 GATGGGGAAAAAGTACCAGAGTGTTTAATTCTGGAGGAGAAGAATAATCAAATTACTTTA 3327

Qy  708 AspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAspGln  727
         |||:::||               |||
Db 3328 GACGTTACG------AACCAAGCAAAGGTTCCTTTACCTGAAAACTGGTGGCATAGGA   3378

Qy  728 LysIleAsnGlyTyrLeuAlaLeuIle---------ValIleAlaGlyIleSerLeuGly  744
         |||                    :::
Db 3379 CGCTTGTTCGGTTTTACTTGATACGGATTAGTAGTACATTCGTGATACGCGGTGTTTTATCTCTTT 3438

Qy  745 Ile                                                   745
         |||
Db 3439 ATT                                                   3441
```

```
Db  2308  GTTCCTCGGTTACAGTCAAGAAAAAATCGACGATACTACTGGAAAAACACGAAGCAGTTC  2367
Qy   291  ThrSerVal------------LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeu  307
                          :::  ::|||
Db  2368  AAGCCATTAGATTTAAAAGATAATCAAAAATTCTTCCTCAGGTGAG------AAAAACTTA  2421

Qy   308  GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe  327
          |||||||
Db  2422  GTGGGAGCCACGCTGCTTTGAATTGAGTGGTAAAAATGTT------CAAACAACATTAGTG  2472

Qy   328  SerSerAsnAsp------------IleGlyArgIleGluSerLysAspGly---Thr  342
                          ::|       |||       :::
Db  2473  GACAATAAAGATGGTTAGCTATTCCTTGCCCAAAAGATGTGCCCTACAAAAAGGGAACGC  2532

Qy   343  TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerValGluAlaGlyIleThrPhe  362
          |||::|||       |||:::|||       |||
Db  2533  TATACATTAACTGAAGTAAAAGCACCTGCAGGACATGAAGTTCAGGAAAAACGACTTGG  2592

Qy   363  LysValGluAla------------GlyLysValTyrThrIleIleAspGlyIleIleGlu  379
          |||||||       |||||||||       ::|||
Db  2593  CAAATTGAGTGAGTGAGCAAGGCAAAGTA------AGCATCGAATGGACAAGAAGTGACC  2646

Qy   380  AsnProAsnLysGlyIleValGluThrTyrSerValGluAlaThrAsnAspProPheGlu  399
          |||::::| -|||       :::|||
Db  2647  ACCACAAAATCAAGTTATT------CCATTGGAAATATGAA------AATAAANTTTCTTCT  2694

Qy   400  PheSerVal------------LeuThrThrGln  410
                          |||       |||
Db  2695  TTGCCAATCAGAATTAGAAAAATACCATTCAAAAAGAAGCTGAACTTACCAGAG  2754

Qy   411  PheThrTyrTyrAla------------LysAsnLysAsnGlySerSerGlnValValTyrCysPhe  427
          ::||||       ||||||||||       |||
Db  2755  GCGACTTTGCGTTGCAAAGAAAAAAAATGCTCAAGGGAAGTTACCAAACGTGGCAACTCAA  2814

Qy   428  AsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrProAsp  447
          |||
Db  2815  AAAACAGAT-  2823

Qy   448  PheThrThrGlyGlyValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThr  467
          ---ACTACAGA-  --
Db  2824  ---ACTACAGA-  2832

Qy   468  ValLysProArgGlyAspThrPheLeuLysHisIleLysLysLysValIleGlu  487
                         |||       ||::       :::
Db  2833  ------------------------TTGAGCTTATTTT---AAAATTAGTGAA  2856

Qy   488  LysGly---TyrArgGlyLysGlyGlnIleAlaIleLeuGluTyrSerGlyLeuThrGluThrGln  506
          |||       :::||||       :::|||       |||
Db  2857  CCTGGTGGAGTATCGA------ATGGTGGAACAATCAGGA---CCA  2892

Qy   507  LeuArgAlaAlaThrGlnIleLeuAlaIleThrTyrTyrPheThrAspSerAlaGluIleAspLys  526
          .||       ||| |||       :::
Db  2893  TTAGGCTACGACACTCTTGCTGGAAATTATGAATTACT------GTTGATAAA  2940

Qy   527  AspLysLeuLysAspTyrHisGlyPheGlyMetAsnAspSerThrLeuAlaValAla  546
                          ::||||
Db  2941  ------------------------TATGGGAAA  2949

Qy   547  LysIleLeuValGluThrTyrAlaGln------------AspSerAsnProProGlnLeuThrAsp  563
          ::|       |||:::|||       |||
Db  2950  ------------ATTCACTATGCACGAAAAAATATTGAAGAAAAATGGGCCAAGAATGACA---  2997

Qy   564  LeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHis  583
                                                 |||||||
Db  2998  ------------------------------CTGACA-  3003

Qy   604  HisAsnLeuThrLeuArgLys------------ThrValThrGlyLeuAlaGlyAspArgThr  620
          |||       |||:::
Db  3004  CATCAAAAAATAATTGAACTTTTGACTAAACAGTTCATAAAAAAAGCCGATAAATCAGACG  3063
```

Alignment Scores:
Pred. No.:
Score: 8.26e-07   Length: 3465
Score: 205.00   Matches: 170
Percent Similarity: 35.37%   Conservative: 85
Best Local Similarity: 23.58%   Mismatches: 236
Query Match: 5.20%   Indels: 231
DB: Gaps: 43

US-09-494-297-2 (1-757) x US-10-434-665-2717 (1-3465)

```
Qy   621  LysAspPhePheHisGlyGluIleLeuLeuLysAsnAsnLysGlyGluLeuLeuSerGlnThr  640
                                         |||       |||
Db  3064  ------------------------CCACTTAAAGAGACGGAAATTCCGTTAACAGGA------  3096

Qy   641  ValLysThrAspLysThrAsnLeuGluPhe------LysAspGlyLysAlaThr---------  656
          |||       |||:::       |||
Db  3097  ---CCAGATACGGATATTGAATTACCAAAAATGGATAAAAACGGATACTTTT------  3147

Qy   657  ------IleAsnLeuLysHisGlyGlu---SerLeuThrLeuGlnLeuProGluGly  673
                    ||||||       :::       |||
Db  3148  GTTTTTGAAAACTTAAAACCAGGAAAATATATGTTCTAACACAGAAGAAACCTTTCACG  3207

Qy   674  TyrSerTyrLeuValLysGlyGluThrAsp------SerGluGlyTyrLysValLysVal  690
          |||       :::       |||:::
Db  3208  TATCAGGGGGTTAAAGGAGACCAATTACCAAAAATAAATTCGTGAGATGTGAGTCAGGATA  3267

Qy   691  AsnSerGlnGluValAlaAlaAsnAlaThrValSer------------LysThrGlyIleThrSer  707
          :::       |||       :::
Db  3268  GATGGGAAAAAAGTAGGACAGTTTAATTTCTGGACAGAAGATAATTACAAAATTACTTTA  3327

Qy   708  AspGluThrLeuAlaPheGluAsnAsnLysGluProValValValProThrGlyValAspGln  727
          |||       :::       |||:::
Db  3328  GACGTTACG------------AACCAAGCAAAAGGTTCCTTTTACCGTGGGGGCATAGGA  3378

Qy   728  LysIleLeuAsnGlyTyrTyrLeuValAlaLeuIle------ValIleAlaGlyIleIleSerLeuGly  744
          :::::       ||||||||||:::
Db  3379  CGCTTGTGGTTTTACTTGATACGGATTAGTACACATTCGTGATAGCGGGTGTTTTTATCTCTTT  3438

Qy   745  Ile  745
          |||
Db  3439  ATT  3441
```

```
Qy    88  PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer------------ArgSerTyrGln  105
          :::       ||||||       :::
Db  1781  TTCAGGTTCAAAACATTA-CCAGAAGTGTCGCTAACAGGCGCTACAATTAATAGTAATGAG  1839

Qy   106  ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys  125
          :::::       |||
Db  1840  ATTTAT------------TTGGGTAAAGGGCCAAGAAAATTCAAATT  1872
```

```
Qy   126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp------            139
                                                                         
Db  1873 CAnTATCAAGTACGT-------AATCAAACAGAGTACAGAAAACTTCAAACCTGATTTTTGG 1926

Qy   140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet  159
         |||| :::   |||  |||  ||| |||    |||
Db  1927 TATCAAATGAATGGTCGGACAAGAGTTGAGTGGAGGAGCCCCTGAAAAAGTTGAT       1986

Qy   160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyValLeuGluProLeuAsnAla 179
         |||                 |||::::
Db  1987 TTT-------GGGGTTCCTTCGGAGAAAAGCACCT------GGC                  2016

Qy   180 IleArgValThrGlnGluLeuAlaValTrpIleTyrSerAspAsnAlaProIleSerAsnPro 199
                      |||     |||||          |||
Db  2017 GTGAAGTTAAACGTGAAAAAAATCTGGAAGAGTATGATCAGAACCCACAAGTCGGCCA    2076

Qy   200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSer             215
         |||              |||:::
Db  2077 GATAAATGTGATTTATGAAAATTAGTAGAAAAGCAAGTAACTGACACAGCCAACT      2136

Qy   216 ------GlnLeuSerLeuMetArgGlnAlaLeuGluSerGlnIleLeuIleAspProAsnLeu 232
              ::::|| |||
Db  2137 GGGTATATTAAATTATCAAGAAAAACCAGAAAATGATTACCAGACAAATAGTTGGGAGGCAAAAT 2196

Qy   233 AlaThrLysMetProLysGlyInValProAlaAspAspPheGln-------LeuSerIlePheGlu 250
                          :::
Db  2197 GTAAACCCAACTTTCCAAAAACCCGGATGAAAAGCTATCACAAGAAGTTCTTGGGCTTCCCAA   2256

Qy   251 SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu     270
         :::|||||           |||||   |||
Db  2257 TACACAACAATCAAGGACAAGCTTTCAAT-------TATCAAACAACCCGTGAATTAGCA-    2307

Qy   271 ValProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThr     290
         ||||||          |||                          :::
Db  2308 GTTCCTCGGTTACAGTCAAGAAAAAAAAATGGACATGACACACATAGTTGGGAGGCAGTTC    2367

Qy   291 ThrSerVal------LeuIleArgLysTyrAlaIleGlyAspTyrSerLysSerLeuLeu     307
         :::         |||  |||
Db  2368 AAGCCATTAGATTTAAAAGTATAACAAAAATTCTTCCTCAGGTGAG-----AAAAACTTA    2421

Qy   308 GluGlyAlaThrLeuGlnIleuThrGlyAspAsnSerPheGlnAlaArgValPhe         327
         |||||       |||                            :::
Db  2422 GTGGGACCCGCTCTTGAATTGGGTTGTAAAAAGTT-------CAAACACATTAGTG       2472

Qy   328 SerSerAsnAsp------IleGlyIleArgIleGluLeuSerAspGly---Thr          342
             :::          |||
Db  2473 GACAATAAAGATGGTAGCTATTCCTTGGCCCAAAAGATGTGCGCCCTACAAAAAGGGAACGC  2532

Qy   343 TyrThrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe  362
         |||||||||||:::||||||||    |||  :::
Db  2533 TATACAATTAACTGAAAGTAAAAGCACCTCCAGAGAACATGAGTTAGGCAAGAAACAGACTTGG 2592

Qy   363 LysValGluAla------GlyLysValTyrThrIleIleuAspGlyLysGlnIleGlu      379
         :::|||||||        ||||||||||
Db  2593 CAAATTGAGGTGGTGAGTGAGCAAGGCAAAGTA-----AGCACTCGATGACAAGAAGTGACC 2646

Qy   380 AsnProAsnLysGluIleuValGlyLeuProTyrSerValGluIleAlaTyrArgAsnAspPheGluGlu 399
         |||:::|||                |||                 :::
Db  2647 ACCACAAAATCAAGTTATT------CCATTGGAAATTGAA-----AATAAATTTCTTCT     2694

Qy   400 PheSerVal------LeuThrThrThrGln------AsnTyrArgAlaLys            410
             :::      |||||||||        ||| :::||||||
Db  2695 TTGCCAATCAGAATTAGAAAAATACACCAGAATTAGAAACAAGTGAACTTAGCACAGAG    2754

Qy   411 PheTyrTyrAla------LysAsnLysAsnGlySerSerGlnValValTyrCysPhe       427
         :::|||         |||||||||
Db  2755 GCCACTTTTGCCTTGCAAAGAAAAAATGCCTCAAGAGAAGTTACCAAACTGTGCAACTCAA   2814

Qy   428 AsnAlaAspLeuLysSerProProAspGluAspGlyIleGlyLysThrMetThrProAsp    447
         |||:::                |||||                |||
Db  2815 AAAACAGAT-------                                             2823

Qy   448 PheThrThrArgThrGlyGluValLysTyrThrHisIleAlaGlyIleArgAspLeuPheLysTyrThr 467
```

```
Db  2824 ---ACTACAGGA---                                             2832
         |||||||||||

Qy   468 ValLysProArgAspThrAspProAspThrPheLeuLeuHisHisIleLeuLysLysValIleLeuGlu 487
                                      |||::: :::
Db  2833 TTGAGCTATTTT---AAAATTAGTGAA                                 2856

Qy   488 LysGly------TyrArgGluLysGlyGlnAlaIleLeuGluThrTyrSerGlyLeuThrGluThrGln 506
         |||      |||::::::                |||||||
Db  2857 CCTGGTGAGTAGTCGA------ATGGTGGAACAACATCAGGA----CCA            2892

Qy   507 LeuArgAlaAlaThrGlnLeuLeuAlaIleTyrTyrTyrPheThrAspSerThrAlaGluLeuAspLys 526
         |||                |||||||||                :::||||||
Db  2893 TTAGGCTACGACACTCTTGCTGGAAATTATGAAATTTACT----GTTGATAAA       2940

Qy   527 AspLysLeuLysAspTyrHisGlyIlePheGlyAspMetAsnAspSerThrArgLeuAlaValAla     546
         |||||||||::: |||||||                  :::
Db  2941 GATAAATTGAAAGATTATCATGGAATATTTGGGGACATGAATGATTCCACTAGATTGGCAGTCGCA   2997

Qy   547 LysLeuLeuValGluTyrAlaGln------AspSerAsnProGlnLeuThrAsp          563
         |||        |||||||    :::||||||
Db  2950 AAACTATGCCAGGCAAAAAATATTGAAAGAAAAATATTGCGGCAAATGCACA---        2997

Qy   564 LeuAspPhePheHisGluLeuLysLysAsnAsnLysTyrGlnSerLeuIleGlyTyrThrGlnTrpHis  583
                                    |||||                 :::
Db  2998 CCAGATACGGATTATTGAATTACCAAAGAAACGGATTACTTTT                  3003

Qy   584 ProGluAspLeuIleIleArgMetGluAspLysLysGlyGluValIleThr            603
                                                      |||||||::: :::
Db  3004 CATCAAAATAATTGAAACCTTTGACTTAACAGTTCATAAGAAAAATTGGAAAAGCGGAAATAATCGGG 3063

Qy   604 HisAsnLeuThrLeuArgLys------ThrValThrGlyLeuLeuAlaGlyAspAspArgThr        620
         |||||||||    |||||    |||        |||
Db  3064 -------CCACTTAAAGGAGGCGAAAATTCCGTTTAACAGGA----                3096

Qy   621 LysAspPhePheHisGluLeuGluLeuLeuSerGlnAsnLysSerGluGlnThr         640
                               |||||||     |||::: |||
Db  3097 ------CCAGATACGGATATTGAATTACCAAAGAAACGGATTACTTTT             3147

Qy   641 ValLysThrAspLysThrAsnLeuGluPhe------LysAspSerGlyLysSerAlaThr--          656
         |||                |||||||           :::
Db  3148 GTTTTTGAAAACTTAAAACCAGGGAAAATATGTTCTAACAGAACCTTTACCGCCAGAAGGA      3207

Qy   657 ------IleAsnLeuLysHisGlyGlu------SerLeuThrLeuGlnGlyLeuProGlyGluGly      673
               ||||||         :::         |||||||
Db  3208 TATCAGGGGTTAAAAGGAACCAAATCGAATTAATTAATTCGTGAAAATGGTTCAGTCACGACGATA   3267

Qy   674 TyrSerThrTyrLeuValLysGluLeuGluThrAsp------SerGluGlyTyrArgLysValVal     690
         |||||||    |||      :::            |||::::
Db  3268 GATGGGGAAAAAGTAGCAGAATGTTTTAATTTCTGGAGAGGAAAATCAAATTACTTTA      3327

Qy   691 AsnSerGlnGluValAlaLysAsnAlaThrValSer------LysThrGlyIleThrSer          707
                           |||                |||::::|||
Db  3328 GACGTTACG------AACCAGCAAAAGGTTCCTTTACCTGAAACTGGTGGCATTAGGA      3378

Qy   708 AspGluThrLeuAlaPheGluAsnAsnLeuGlyProValProThrGlyValAspGln          727
                          |||:::             |||
Db  3379 CGCTTGCTGGGTTTTACTTGATTAGCGGATTTAGTACAATTCGTTTTA TCTTT        3438

Qy   728 LysIleLeuAsnGlyTyrTyrLeuGlnAlaLeuLeuIleLeu------ValIleLeuAlaGlyIleSerLeuGly 744
         |||               |||           ||||||||||| :::
Db  3439 ATT                                                         3441

Qy   745 Ile                                                        745
         |||
Db  3439 ATT                                                        3441
```

RESULT 7
US-09-070-927-45
Sequence 45, Application US/09070927

APPLICANT: Steven C. Barash
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15614 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-070-927-45

Alignment Scores:
Pred. No.:
Score: 196.00
Percent Similarity: 35.578
Best Local Similarity: 23.11%
Query Match: 4.978
DB: 15

US-09-494-297-2 (1-757) x US-09-070-927-45 (1-15614)

Length: 15614
Matches: 165
Conservative: 89
Mismatches: 245
Indels: 216
Gaps: 41

```
Qy   88  PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer------ArgSerTyrGln  105
             ||||||   |||   |||::   ||:   |||   ||||    ||::
Db  9047  TTCAGGTCAAACATTA--CCAGAAGTGTCGCTACACAGGCGCCTACAATTAATAGTAATGAG  9105

Qy  106  ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys  125
             ||||||            |||                        ::::::
Db  9106  ATTTAT--------------------------------------TTGGGTAAAGGCCAAGAAAATTCAAATT  9138

Qy  126  TrpIleTyrLysLysHisAspGlyIleSerThrLysPheGluAsp------------  139
             || |||::||   |   |||::   |||
Db  9139  CATTATCAAGTACGT------ATTCAAACAGAGTCAGAAAACTTCAAACCTGATTTTTGG  9192

Qy  140  TyrAlaMetSerProArgIleThrGlyAspGluAsnGlnLysLeuArgAlaValMet  159
             ||||||   ||:::   |||   |||   |::||
Db  9193  TATCAAAATGAATGGTCGGACAACGTTTCAGCCATTAGCCACGGCGCCCTGAAAAGTTGAT  9252

Qy  160  TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla  179
             |||:::            ||||||            :||
Db  9253  TTT----------------------GGGGTTCCTTCGGGAAAAGCACCT----GGC  9282

Qy  180  IleArgValThrGlnGluAlaValThrProTyrTyrSerAspAsnAlaProIleSerAsnPro  199
             :::   |||||||   |||
Db  9283  GTGAAGTTAAACGTGAAAAAAATCTGGGAAGAGTATGATCAAGACCGACAAGTCGGCCA  9342

Qy  200  AspGluSerPheLysArgGluSerAsnLeuValSerThrSer------------  215
             :::||||
Db  9343  GATAAATGTGATTTATGAAATTGAAATTAGTAGAAGCAGAGCAAGTAACTGACAGCGCAAACT  9402
```

```
Db  9403  GGGTATATTAAATTATCAAAACCAGAAAAATGATACCAGCAATAGTTGGGAGCCGCAAAAAT  9462

Qy  233  AlaThrLysMetProLysGlnValProAspAspPheGln------LeuSerIlePheGlu  250
             ||||::            |||            ||   :::
Db  9463  GTAACCCAAACTTTCCAAAACCCGGAGAAACCTATCAAAGAAGTTCTTGGGCTTCCCAA  9522

Qy  251  SerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu  270
             :::   ||||||   ||::   |   :::   |||
Db  9523  TACAACAATCAAGGACAGCAAGCTTCAAT-----TATCAAACAACCCGTGAATTAGCA-  9573

Qy  271  ValProThrLysProProThrProGlyAspProMetProProAsnGlnThr  290
             ||||||         |||||||         |||
Db  9574  GTTCCTGGTTACAGTCAAGAAAAAATCGACGATACTACTTGGAAAACACGAGAGCAGTTC  9633

Qy  291  ThrSerVal------LeuIleArgLysTyrAlaIleIleGlyValGlyLeuLeu  307
             ::|||                   |||
Db  9634  AAGCCATTAGATTTAAAAGTAATCAAAAAATTCTTCCCGCAGGTGAG------  9687

Qy  308  GluGlyAlaThrLeuGlnIleLeuThrGlyAspAspAsnValAsnSerPheGlnIleAlaArgValPhe  327
             ||||||            |::||   |||   :::   |||
Db  9688  GTGGGAGCGCCGTCTTTGAATTGACTGGTGATAAATGTT------CAAACAACATTAGTG  9738

Qy  328  SerSerAsnAsp------------IleGlyGluArgIleGluLeuSerAspGly--Thr  342
             :::||   |||                   |||
Db  9739  GACAATAAAGATGGTAGCTATTCCTTGCAAAAAGATGTGCGCCTACAAAAAAGGGAACGC  9798

Qy  343  TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrTyrSerIleAlaGluProIleThrPhe  362
             ||||||||||||||||||            |::   |||
Db  9799  TATACATTAACTGAAGTAAAACCACCTGCAGACATGAGTTAGGCAGAAAACGACTTGG  9858

Qy  363  LysValGluAla------GlyLysValThrIleIleLeuAspGlyLysGlnIleGlu  379
             :::||||||            |::
Db  9859  CAAATTGAGGTGAGTGAGCAAGGCAAAGTA------AGCATCGATGGACAAGAGTGACC  9912

Qy  380  AsnLysAsnGlySerSer-GlnValValTyrCysPheAsnAlaAlaAspLeuLysSerProArg  435
             :::            |::   |||
Db  10003 CAAGTGAACTTAGCAGAAGGCGACTTTTTGCGTTCCAAAGAA----------  10042

Qy  400  PheSerVal------LeuThrThrArgGlnAsnTyrAlaAlaLysPheThrTyrTyrAlaLys  415
             |::||
Db  9913  ACCACAAATCAAGTATT------CCATTGGAAATTGAA------AATAAATTTTCTTCT  9960

Qy  416  AsnLysAsnGlySerSer-GlnValValTyrCysPheAsnAlaAlaAspLeuLysSerProArg  435
             :::            |::   |||
Db  9961  TTGCCAATCAGAATTAGAAAAAATTACACACATGCAAAAT------GGCAAA  10002

Qy  435  oAspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTy  455
             |::||            |||
Db  10043 ------------------AAAATGCTGCAAGGAAGTTACCAAACTGTGGCAACTCAAAA  10083

Qy  455  rThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPr  475
             |||            |||
Db  10084 AACAGATACTACAGGATTGAGCTATTTT----------------  10111

Qy  475  oAspThrPheLeuLysHisIleAlaTyrIleLeuValLysValIleGluLeuLysSerGly-  494
             |::::::            |::
Db  10112 ------------------AAAATTAGTAGAACCTGGTGAGTATCGA------  10138

Qy  494  yGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAl  514
             :::||:||::            |||
Db  10139 ----ATGGTGGAACAATCAGGA------CCATTAGGCTACGGACAACTCTTGCCTGCTGG  10182

Qy  514  aIleTyrTyrPheThrAspSerAlaGluLeuAspLysSerLeuLysAspTyrHisSgI  534
             ::::::            |||
Db  10183 AAAATTATGAAATTTACT-------------------GTTGATAAA-----  10207

Qy  534  yPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGl  554
             ::::|||
```

RESULT 8
US-09-070-927A-45
Sequence 45, Application US/09070927A
GENERAL INFORMATION:
  APPLICANT:
    APPLICANT: Charles A. Kunsch
              Patrick J. Dillon
              Steven Barash
  TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
  NUMBER OF SEQUENCES: 982
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Human Genome Sciences, Inc.
    STREET: 9410 Key West Avenue
    CITY: Rockville
    STATE: Maryland
    COUNTRY: USA
    ZIP: 20850
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
    COMPUTER: HP Vectra 486/33
    OPERATING SYSTEM: MSDOS version 6.2
    SOFTWARE: ASCII Text
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/070,927A
    FILING DATE: 04-May-2000
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/046,655
    FILING DATE: 1997-05-16
    APPLICATION NUMBER: 60/044,031
    FILING DATE: 1997-05-06
    APPLICATION NUMBER: 60/066,009
    FILING DATE: 1997-11-14
  ATTORNEY/AGENT INFORMATION:
    NAME: Kenley K. Hoover
    REGISTRATION NUMBER: 40,302
    REFERENCE/DOCKET NUMBER: PB369
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (301) 309-8504
    TELEFAX: (301) 309-8512
  INFORMATION FOR SEQ ID NO: 45:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 15614 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-070-927A-45

US-09-494-297-2 (1-757) x US-09-070-927A-45 (1-15614)

Alignment Scores:
  Pred. No.:   3.46e-05   Length: 15614
  Score: 196.00   Matches: 165
  Percent Similarity: 35.57%   Conservative: 89
  Best Local Similarity: 23.13%   Mismatches: 245
  Query Match: 4.97%   Indels: 216
  DB: 15   Gaps: 41

Qy 554 n-------AspSerAsnProGlnLeuThrAspLeuAspPhePheIleProAsnAs 571
Db 10208 -TATGGGAAA-------ATTCACTATGCAGG 10230

Qy 571 nAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIl 591
Db 10231 CAAAAATATTGAAGAAAATGGCCCAGAATGGACA 10264

Qy 591 eArgMetGluAspLysLysGlyLeuValIleProValThrHisAsnLeuThrLeuArgLys-- 610
Db 10264 ... 10264

Qy 611 -------ThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGl 628
Db 10265 -------CTGACACATCAAAATAATTGAAACCTTT 10293

Qy 628 uLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLe 648
Db 10294 TGACTTAACAGTTAATAAAAAGCCGATAATCAGACG--CC 10332

Qy 648 uGluPhe---LysAspGlyLysAlaThr------IleAsnLeuLysHisG1 662
Db 10333 ACTTAAAGGAGCGAAAATTCCGTTTAACAGGA------CCAGAATACGGATAT 10377

Qy 662 yGlu---SerLeuThrLeuGlnGlyLeuProGluGlyThrTyrSerTyrLeuValLysGluTh 681
Db 10378 TGAATTACCAAAAGATGGCCAAAGAAACGGATACTTTTGTTTTGAAAACTTAAAACCAGG 10437

Qy 681 rAsp-------SerGluGlyTyrLysValLysValAsnSerGlnGluValAlaAsnAl 698
Db 10438 GAAATATGTTCTAACAGAAACCTTTACGCACGAAGGATATATCAGGGGTTAAAAGAACCAAT 10497

Qy 698 aThrValSer--------LysThrGlyIleThrSerAspGluThrLeuAlaPheGluAs 715
Db 10498 CGAATTAAATAAATTCGTTCAAGACGGTTCAGTCACGATAGATGGGGAAAAAGTAGCAGAtGT 10557

Qy 715 nAsnLysGluProValValProThrGlyValAspSerGlyLysIleAsnGlyTyrTyrLeuAla 735
Db 10558 TTTAATTCTCGGAGAAGAATAAATACAAATTACTTAGACGTTACG---AACCA 10608

Qy 735 uIle-------ValIleAlaGlyIleSerLeuGlyIle 745
Db 10609 AGCAAAAGGTTCCTTTACCTGGGCATAGGACGCGTTGGTTTTACTTGATAGC 10668

Db 10669 GATTAGTAGACATTCGTGATAAGCCGGGTGTTTTATCTCTTTATT 10708

Qy 88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer-----ArgSerTyrGln 105
Db 9047 TTCAGGTTCAAAACATTA-CCAGAAGTGTCGCTTACCAGGCCGCCTACAAATTAATAGTAATGAG 9105

Qy 106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys 125
Db 9106 ATTTAT-TTGGGTAAAGGCAAGAAAATTCAAATT 9138

Qy 126 TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp--- 139
Db 9139 CATTATCAAGTACGT---ATTCAAACAGAGTCAGAAAAACTCAAACCTGATTTTTGG 9192

Qy 140 TyrAlaMetSerProArgIleThrGlyAspGlyLeuAsnGlnLysLeuArgAlaValMet 159
Db 9193 TATCAAAATGAATGGTCGGACAACGTTTCAGCCATTAGCACGGCCCCTGAAAAAGTTGAT 9252

Qy 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlyGlyLeuGluProLeuAsnAla 179
Db 9253 TTT---GGGGTTCCTTCGGGAAAAGCACCT---GGC 9282

Qy 180 IleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db 9283 GTGAAGTAAACAGTGAAAAAAATCTGGGAAGAGTAGATAACCGACAAGGTCGGCCA 9342

Qy 200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSer------- 215
Db 9343 GATAATGTGATTATGAAATTAGTAGAAAGCAAGTAACTGACACAGCCAACTGGCAAACT 9402

Qy 216 ------GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleLeuAspProAsnLeu 232
Db 9403 GGGGTATATTAAAATTATCAAAACCAGAAAAATGATACCAGAAATAGTTGGGAGCGCAAAAAT 9462

Qy 233 AlaThrLysMetProLysGlnValProAlaSerProPheGln------LeuSerIlePheGlu 250
Db 9463 GTAACCCACTTTCCAAACCGCGGATGAAAGC...ATCAGAAGTTCTTGGGCTTCCCAA 9522

Qy 251 SerGluAspLysGlyAspLysTyrAsnLysGlyLysTyrGlnAsnLeuLeuSerGlyGlyLeu 270
Db 9523 TACAACAAATCAAGGACAAGCTTTCAAT-----TATCAAACAACCCGTGAATTAGCA--- 9573

Qy 271 ValProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThr 290

```
Db   9574 GTTCCTGGTTACAGTCAAGAAAAAATCGACCATACTACTTGGAAAAACACGAAGCAGTTC 9633
Qy    291 ThrSerVal------LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeu       307
Db   9634 AAGCCATTAGATTTAAAAGATTAATCAAAAAATTCTTCCTCAGGTGAG------AAAACTTA 9687
Qy    308 GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe   327
Db   9688 GTGGGAGGCCGTCTTTGAATTGAGTGGTAAAAATGTT------CAAACAACATTAGTG     9738
Qy    328 SerSerAsnAsp------IleGlyGluArgIleGluLeuSerAspGly---Thr        342
Db   9739 GACAATAAAGATGGTAGCTATTCCTTGCCAAAAAGATGGTGCCCCTACAAAAAGGGAACGC 9798
Qy    343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe   362
Db   9799 TATACATTACTGAAGTAAAAGCACCTGCCAAGCATGAGTTAGGCAAGAAAACGACTTGG   9858
Qy    363 LysValGluAla------GlyLysValTyrThrIleIleAspGlyLysGlnIleGluGlu   379
Db   9859 CAAATTGAGGTGAGTGAGCAAGGCAAAGTA------AGCATCGATGGACAAGAAGTGACC  9912
Qy    380 AsnProAsnLysGluLeuValGluProTyrSerValGluAlaThrPheAsnAspPheGluGlu 399
Db   9913 ACCACAAAATCAAGTTATT------CCATTGAAAATTGAA------AATAAAATTTCTTCT 9960
Qy    400 PheSerVal------LeuThrThrGlnAsnTyrArgLeuAlaLysPheTyrTyrAlaLys   415
Db   9961 TTGCCAATCACAGAAATTGAAAATACACCATCGCAAAAT------GGCAAA           10002
Qy    416 AsnLysAsnGlySerSer-GlnValValTyrCysPheAsnAlaAspLeuLysSerProPr   435
Db  10003 CAAGTGAACTTAGCAGAGGCGACTTTGCGTTGCAAAGAA                       10042
Qy    435 oAspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyLeuValLysTy   455
Db  10043 ------AAAATGCTGCAAGGAAGTTACCAAACTGTGGCAACTCAAAA                10083
Qy    455 rThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPr   475
Db  10084 AACAGATACTACAGGATTGAGCTATTT                                   10111
Qy    475 oAspThrPheLeuLysHisIleLeuLysValIleGluLysGly---TyrArgGluLysGly 494
Db  10112 ------AAAATTAGTGAAACCTGGTGAGTATCGA------                      10138
Qy    494 yGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAl   514
Db  10139 ------ATGGTGGAACAAATCAGGA------CCATTAGGCTACGAACACTCTTGCCTGG  10182
Qy    514 aIleTyrTyrPheThrAspSerAlaGluLeuAspLysSerAspLysSerAspTyrHisGl   534
Db  10183 AAATTATGAATTTACT------GTTGATAAA                               10207
Qy    534 yPheGlyAspMetAsnAspSerThrLeuLeuAlaLysIleLeuValGluTyrAlaGl     554
Db  10208 -TATGGGAA------ATTCACTATTGCAGG                                10230
Qy    554 n------DspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAs     571
Db  10231 CAAAAATATTGAAGAAAATCGGCCAGAATGGACA------                      10264
Qy    571 nAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIl   591
Db  10265 ------CTGACACATCAAAAATAATTTGAAACCTTT                          10293
Qy    591 eArgMetGluAspLysLysGluValIleProValThrHisIleAsnLeuThrLeuArgLys-- 610
Db  10294 TGACTTAACAGTTAATAAAAAAGCCGATAATCAGACG------CC                 10332
Qy    611 ------ThrValThrGlyIleLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGl 628
Qy    628 uLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnIle 648
Db  10333 ACTTTAAAGGAGGCGAAATTCCGTTTAACAGGA------                       10377
Qy    648 uGluPhe------LysAspGlyLysAlaThr------IleAsnLeuHisGl           662
Db  10378 TGAATTACCAAAAGATGGCAAAGAAAACGGATACTTTGTTTTGAAAACTTAAAACCAGG  10437
Qy    662 yGlu---SerLeuThrLeuGlnGlyLeuProGluGlyValTyrSerTyrLeuValLysGluTh 681
Db  10438 GAAATATGTTTCTAACAGAGAAACCTTTACGCACAGAAGGATATCAGGGGTTAAAAGAACCAAT 10497
Qy    681 rAsp------SerGluGlyTyrLysValLysAsnSerGlnGluValAlaAsnAl        698
Db  10498 CGAATTAAATAATTCGTGAAGATGGTTCAGTCACGATACAGTGGGAAAAAAGTAGCCAGATGT 10557
Qy    698 aThrValSer------LysThrGlyIleThrSerAspGluThrLeuAlaPheGluAs     715
Db  10558 TTTAATTTCTTGGAGGAAGAAATAATCAAATTACTTTAGACAGTTACG------AACCA  10608
Qy    715 nAsnLysGluProValValProThrGlyValAspGlnLysIleAsnGlyIleTyrLeuAlaLe 735
Db  10609 AGCAAAGAGGTTCCTTTACCTGAAACTGGTGGCCATAGGACCCTTCGTGGTTTTACTTGATAGC 10668
Qy    735 uIle------ValIleAlaGlyIleSerLeuGlyIle                         745
Db  10669 GATTAGTACATTCGTGATAGCGCGGGTGTTTATTCTCTTTATT                  10708
```

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:

3.29e-05
192.00
33.65%
23.15%
4.87%
58

Length: 7971
Matches: 172
Conservative: 78
Mismatches: 220
Indels: 274
Gaps: 42

DB:

US-09-494-297-2 (1-757) x US-60-045-649-1048 (1-7971)

RESULT 10
US-60-046-653-1042
Sequence 1042, Application US/60046653

GENERAL INFORMATION:
APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Neil C.
APPLICANT: Russo, Frank D.
APPLICANT: Hann, Amy L.
APPLICANT: Heath, Joe D.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1449
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/046,653
FILING DATE: HEREWITH
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0003-1 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 1042:
SEQUENCE CHARACTERISTICS:
LENGTH: 8040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: EFA1c1042

US-60-046-653-1042

Alignment Scores:

Pred. No.:	3.32e-05	Length:	8040
Score:	192.00	Matches:	172
Percent Similarity:	33.65%	Conservative:	78
Best Local Similarity:	23.15%	Mismatches:	220
Query Match:	4.87%	Indels:	274
DB:	58	Gaps:	42

US-09-494-297-2 (1-757) x US-60-046-653-1042 (1-8040)

```
Qy   689 sValAsnSerGlnGluValAlaAlaAsnAlaThrValSer------LysThrGlyIleTh 706
             :::|||||||||||||||||
Db  3133 GATAGATGGGGAAAAAGTAGCAGAtGTTTTAATTTCTGAGAGAGAAGAAATCAAATTAC 3192

Qy   706 rSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs 726
             ||| |||  |||    ||| |||
Db  3193 TTTAGACGTTACG------AACCAAGCAAAGGTTCCTTTACCTGAAACTGGTGGCAT 3243

Qy   726 pGlnLysIleAsnGlyTyrTyrLeuAlaLeuIle------ValIleAlaGlyIleSerLe 743
             ||||| |  |||||    |||||||||:|:| |||
Db  3244 AGGACGCTTCGTGGGTTTTACTTGATAGCGATTAGTACATTCGTGATAGCGGGGTGTTTATCT 3303

Qy   743 uGlyIle 745
             |||
Db  3304 CTTTATT 3310
```

```
Qy    88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer------ArgSerTyrGln 105
             |||||||||| |||||||| ||:::|||  |||    :::
Db  1718 TTCAGGTTCAAACATTA-CCAGAAGTCTCGCTACAGCGGCTACAATTAATAGTAAGAG 1776

Qy   106 ValThrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys 125
             ::|||||  |||||     |||||||  :::
Db  1777 ATTTAT------TTGGGTAAAGGGAAGAAATTCAAATT 1809

Qy   126 TrpIleLysLysHisAspGlyIleIleSerThrLysPheGluAsp------ 139
             ||||| | :::      ||| |||:::  |||
Db  1810 CATTATCAAGTACGT------ATTCAAACAGAGTCAGAAAACTTCAAAACCTGATTTTGG 1863

Qy   140 TyrAlaLaMetSerProArgIleThrGlyAspLeuAspGluValLeuArgAlaValMet 159
             ||| :::      ||| |||      |||  |||
Db  1864 TATCAAAATGAATGGTCCGGACAACGTTTCAGCCATTACCACGCCCCCTGAAAAAGTTGAT 1923

Qy   160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyIleLeuGluProLeuAsnAla 179
             |||  :::
Db  1924 TTT------GGGGTTCCTTCGGGAAAAGCCACCT-GGC 1953

Qy   180 IleLeuArgValThrGlnIleLeuValAlaValTrpIleTyrTyrSerAspAsnAlaProIleSerAsnPro 199
             :::||| ||| ||| |||
Db  1954 GTGAAGTTAAACGTGAAAAAAATCTGGAAGAGAGTGAAGCGACAAGTCGGCCA 2013

Qy   200 AspGluSerPheLysArgGluSerGluAsnLeuValSerThrSerGlnIleLeuSerLeu 219
             |||      :::
Db  2014 GATAAATGTGATTTATGAAATTAGTAGAAGAAGCAAGTAACTACACAGCCAAC------ 2064

Qy   220 MetArgGlnIleAlaLeuLeuLysGlnLeuIleLeuAspProAsnLeuAlaThrLysMetProLysGln 239
             |||     |||
Db  2065 TGGCAAACTGGGTATTATAAATTATCAAAACCAGAAAAATGATAACCAGCAATAGTTGGGAG 2124

Qy   240 ValProAspPhePheGlnLeuSerIlePheGluSerGluAsnLysGlyAspLysTyrAsn 259
             :::
Db  2125 CGCAAAAATGTTAACCCAACTTTCCAAAAACCCGGGATGAA------ 2163

Qy   260 LysGlyTyrGlnAsnLeuSerGlyGlyLeuValProThrProProThrProGly 279
             |||||| :::|||
Db  2164 ------AGCTATTCAAGAAGTTCTTGGG 2184

Qy   280 AspProProMetProProAsnGlnProGlnThrThrSerValLeuIle------ 296
             :::|||||| :::
Db  2185 ------CTTCCCCAATACAACAATCAAGGACAACAAGCTTTCAATTATCAAAACAACCCG 2235

Qy   296 glyLysTyrAlaIleGlyAspTyrSer------ 304
Db  2236 TGAATTAGCAGTTCCTGGTTCACAGTCAAGAAAAAATCGACAGTACTACTTGGAAAAACAC 2295

Qy   305 ------LysIe 306
             ||
Db  2296 GAAGCAGTTCAAGCCATTAGAATTAGATTAAAAGTAATCAAAAATTCTTCCTCAGGTGAGAAAA 2355

Qy   306 uLeuGluGlyAlaThrLeuGlnLeuGlyAspAsnValAsnSerPheGlnAlaArgVa 326
             :::||||||||| :::||| |||
Db  2356 CTTAGTGGGACCGTCTTTGAATTGAGTGGTAAAAGTGTT------CAAACAACATT 2406

Qy   326 lPheSerSerAsnAsp------ 341
             :::||| :::
Db  2407 AGTGGACAATAAAAGATAGTTAGCTATTCCTTGCCAAAAGATGGGTGCGCCTACAAAAAAGGGA 2466

Qy   342 -ThrTyrThrLeuThrGluLeuAsnSerProLeuAlaGlyTyrSerIleAlaGluProIleTh 361
             |||||| ::: :::|||
Db  2467 ACGCTATTACATTAACTCAAGTAAAAGCACCTCCAGGACACATGAGTTAGGCAAGAAAACGAC 2526

Qy   361 rPheLysValGluAla------GlyLysValTyrThrIleIleAspGlyLysGlnIl 378
             |:::::: :::||| |||
Db  2527 TTGGCAAAAATTGAGGTGAGTGAGCAAGGCAAAGTA------AGCACGGATGGAACAAGAAGT 2580

Qy   378 eGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrArgAsnAspPheGl 398
             |||||| :::||| :::
Db  2581 GACCACCACAAAATCAAAGTTATT------CCATTGGGAAATTGAA------AATAAAATTTTC 2628

Qy   398 uGluPheSerVal------LeuThrThrGln------AsnTyrAl 409
             :::
Db       GACCACCACAAAATCAAAGTTATT------LeuThrThrGln 2628
```

```
Db  2629  TTCTTGCCAATCAGAATTAGAAAATACACCATGCAAAATGGCAAACAAGTGAACTTAGC  2688
                :::                                |||              |||
Qy   409  aLysPheTyrTyrAla---------LysAsnLysAsnGlySerSerGlnValTyrCy   426
                |:||                     |||||

Db  2689  AGAGGCGGACTTTTGCGTTGCAAAGAAAAATGCTCAAGGAAGTTACCAAACTGTGGCAAC  2748
Qy   426  sPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrPr  446
          |||

Db  2749  TCAAAAAACAGAT------------------------  2761
Qy   446  rThrValLysProArgAspThrAspProAspThrPheLeuLysHisIleLeuLysLysValIl  466
               |||

Db  2762  ---ACTACAGGA---------------------------  2770
Qy   466  oAspPheThrThrGlyLeuValLysTyrThrHisIleLeuAlaGlyArgAspLeuPheLysTy  486
              |||||||

Db  2771  TTGAGCTATTTT---AAAATTAG  2790
Qy   486  eGluLysGly---TyrArgGluLysGlyGlnAlaIleLeuGluTyrSerGlyLeuThrGluTh  505
              |||          :|||

Db  2791  TGAACCTGGTGAGTACGA-------ATGGTGGAACAAATCAGGA--  2827
Qy   505  rGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuS  525
              |||||                |||||||

Db  2828  -CCATTAGGCTACGACACTCTTGCCTGGAAATTATTGAAATTTACT---GTTGA  2874
Qy   525  plysAspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaVa  545
              |||                    |||||||

Db  2875  TAAA---------------TATGGGAAA-------  2887
Qy   545  lAlaLysIleLeuValGluTyrAlaGln---AspSerAsnProProGlnLeuTh  562
              ||||||            :::

Db  2888  ATTCACTATGCAGGCAAAAATATATTGAAGAAAATGCGCCAGAAATGGAC  2934
Qy   562  rAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTr  582
          |:|||||

Db  2935  A----  2935
Qy   582  pHisProGluAspLeuValAspIleIleArgMetGluAspLysLysGluValIleProVa  602
              :::

Db  2936  .---CT  2937
Qy   602  lThrHisAsnLeuThrLeuArgLys---ThrValThrLysAspPheHisPheGluIleGlyAspAr  619
              |||

Db  2938  GACACACCAAAAATAATTTGAAACCTTTGACTTAACAGTTCATTAAAAAAGCCGATAATCA  2997
Qy   619  gThrLysAspPheHisPheGluIleLeuLeuLysAsnLysGlnGluLeuLeuSerGl  639
              |

Db  2998  GACG---CCACTTAAAGGAGGAGCGAAATTCCGTTTAACAGGA-  3034
Qy   639  nThrValLysThrHisAspLysLeuGluPhe------LysAspGlyGlyLysAlaThr  656
              |||

Db  3035  -----------CCAGATACGGATATTGAATTACCCAAAAGATGGCAAAGAAACGGATAC  3081
Qy   657  ----IleAsnLeuHisGlyGlu--SerLeuThrLeuGlnGlyLeuProGl  672
              |||||||     |:::

Db  3082  TTTTGTTTTGAAAACTTAAAACCAGGGAAAATAATGTTCTACAGAAAACCTTTACGCCAGA  3141
Qy   672  uGlyTyrSerTyrLeuValLysGluThrAsp--------SerGluGlyTyrLysLysValLy  689
              |||||

Db  3142  AGGATATCAGGGGTTAAAAGAACCAATGAATAATTCCGTAGAAGATGGGTTCAGTCAC  3201
Qy   689  sValAsnSerGlnGluValAlaAsnAlaThrValSer--------LysThrGlyIleTh  706
              ::::::||||:|||:::

Db  3202  GAtAGAGTGGGGGAAAAAGTAGCAGATGTTTAATTCTGGAGAGAGAATAAATCAAATTAC  3261
Qy   706  rSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs  726
              |||

Db  3262  TTTAGACGTTACG---  3312
Qy   726  pGlnLysIleAsnGlyTyrLeuuAlaLeuIle------ValIleAlaGlyIleSerIle  743
              |||||                              ||||||||||:::    ||

Db  3313  AGGACGGCTTGCTGTGGTTTTACTTGATGATAGCGATTAGTAGTACATTCGTGATAGCGGTGGGTGTTTATCT  3372
Qy   743  uGlyIle  745
              |||

Db  3373  CTTTATT  3379
```

RESULT 11

US-60-068-217-919

Sequence 919, Application US/60068217
; GENERAL INFORMATION:
APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Neil C.
APPLICANT: Russo, Frank D.
APPLICANT: Hann, Amy L.
APPLICANT: Heath, Joe D.
APPLICANT: Finney, Gregory L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1239
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/068,217
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0003-5 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 919:
SEQUENCE CHARACTERISTICS:
LENGTH: 11907 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLONE: EFA1c919
US-60-068-217-919

Alignment Scores:
Pred. No.:
Score: 192.00
Percent Similarity: 33.65%
Best Local Similarity: 23.15%
Query Match: 4.87%
DB: 60

US-09-494-297-2 (1-757) x US-60-068-217-919 (1-11907)

Length: 11907
Matches: 172
Mismatches: 78
Conservative: 220
Indels: 274
Gaps: 42

Score: 5.48e-05

```
Db  5455  TTCAGGTTCAAACATTA-CCAGAAGTGTCGCTAACAGGCGCTACAATTAATAGTAATGAG  5513
Qy   106  ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys  125
              |||||

Db  5514  ATTTAT-------------TTGGGTAAAAGGGCAAGAAAATTCAAATT  5546
Qy    88  PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer-----ArgSerTyrGln  105
              ::::::|||||:||

Qy   126  TrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp------------------  139
```

Db 5547 CATTATCAAGTACGT-----ATTCAAACAGAGTCAGAAAACTTCAAACCTGATTTTTGG 5600

Qy 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
     |||:::
Db 5601 TATCAAATGAATGGTGGACAACGTTTCAGCCACGGCCCCTGAAAAAGTTGAT 5660

Qy 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179
     |||
Db 5661 TTT------------GGGGTTCCTTGCGGGAAAAGCCACT- 5690

Qy 180 IleArgValThrGlnGluAlaLeuValalaTrpTyrTyrSerAspAsnSerAlaProAsnPro 199
     :::|||||:::
Db 5691 GTGGAAGTTAAACGTGAAAAAATCTGGGAAGAGTATGATCAAGGAGACCCGACAAGTCGGCCA 5750

Qy 200 AspGluSerPheLysArgGluSerGlyLeuValSerThrSerGlnLeuSerLeu 219
     ||||||
Db 5751 GATAAATGTGATTTATGAAAATTAGTAGAAAAGCAAGTAACTGACAGCCAAC- 5801

Qy 220 MetArgGlnAlaAlaLeuLysGlnLeuIleLeuAspProAsnLeuAlaThrLysMetProLysGln 239
     ||| :::|||
Db 5802 TGGCAAACTGGGTATATTAAATTATCAAAAACCAGAAAATGATACCAGCAATAGTTGGGAG 5861

Qy 240 ValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsn 259
     |||||||||
Db 5862 CGCAAAAAATGTAACCCAACTTTCCAAAACCGGGATGAA------ 5900

Qy 260 LysGlyThrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrProGly 279
     :::
Db 5901 ---AGCTATCAAGAAGTTCTTGGG--------- 5921

Qy 280 AspProProMetProProAsnGlnThrThrSerValLeuIle------ 296
     :::|||||||||
Db 5922 ------CTTCCCCAATACACAATCAAGGACACGACTTTCCAAATTATCAAACAACCG 5972

Qy 296 glyLysTyrAlaIleGlyAspTyrSer------ 304
     :::
Db 5973 TGAAATTAGCACAGTTCCTTGGGTTACAGTCAAGAGAAAAATCGACGTACTACTTGGAAAAACAC 6032

Qy 305 ------ 306
Db 6033 GAAGCAGTTCAAGCCATTAGATTTAAAAGTAATCAAAAATTCTTCCTCAGGTGAGAAAAA 6092

Qy 306 uLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgVa 326
     |||||||||||
Db 6093 CTTAGTGGGAGCGCCGTCTTTGAATTGAGTGGTAAAAATGTT------ 6143

Qy 326 IPheSerSerAsnAsp------ 341
     |||
Db 6144 AGTGGACAATAAAGATGGTAGCTATTCCTTGCCAAAAGATGTGCGCCTACAAAAAGGGA 6203

Qy 342 -ThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleIleAlaGluProIleTh 361
     :::|||||||||:::
Db 6204 ACGCTATACAATTACAGCAAGAAGGCCACCTGCAGTTAGGCAAGAAAAACGAC 6263

Qy 361 rPheLysValGlyAla------ 378
     |||||||
Db 6264 TTGGCAAATTGAGGTGAGTGAGCAAGGCAAAGTA----- 6317

Qy 378 eGluAsnProAsnLysGlyIleValGluProTyrSerValAlaTyrAsnAspPheGl 398
     |||
Db 6318 GACCACCACAAATCAAGTTATT------CCATTGGAAATTGAA 6365

Qy 398 uGlyPheSerVal------ 409
     :::|||
Db 6366 TTCTTTGCCAATACAGAATTAGAAAAATACACAATCTAGAAAAATTAGACCTGGAAAACAC 6425

Qy 409 aLysPheTyrTyrAla- 426
     :::
Db 6426 AGAGGCGGACTTTTGCGTTGCAAAGAAAAAAAATGCTCAAGAGAAGTTACCAAACTGTGGCCAAC 6485

Qy 426 sPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrPr 446
     ||||
Db 6486 TCAAAAAACAGAT----------- 6498

Qy 446 oAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTy 466
     ||||||||||
Db 6499 -------ACTACAGGA--------- 6507

Qy 466 rThrValLysProArgAspThrAspProAspThrPheLeuHisIleLysLysLysValIl 486
     ||||
Db 6508 -----TTGAGCTATTTT----AAAATTAG 6527

Qy 486 eGluGlyGly---TyrArgGlyLysGlyGlnAlaIleLeuGluTyrSerGlyLeuThrGlyTh 505
     ||| |||||:::||
Db 6528 TGAACCTGGTGAGTGATATCGA-------ATGGTGGGAACAATCAGGA---- 6564

Qy 505 rGlnLeuArgAlaAlaThrGlnLeuAlaIleLeuTyrThrPheThrAspSerAlaGluLeuAs 525
     |||||||||||||
Db 6565 -CCAATTAGGCTACGACACTCTTCCTCTGGAAATTATGAAATTTACT------GTTGA 6611

Qy 525 pLysAspLysLeuLysLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAla 545
     :::
Db 6612 TAAA------------TATGGGAAA 6624

Qy 545 lAlaLysIleLeuValGluTyrAlaGln------ 562
     |||||||AspSerAsnProProGlnLeuTh
Db 6625 ---------ATTCACTATGCAGGCAAAAAATATTGAAGAAAGACCCGATAATCA 6671

Qy 562 rAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGln 582
     |||||
Db 6672 A--------CCACTTAAAAGGAGCGAAATTCCGTTTAACAGGA-- 6671

Qy 582 pHisProGluAspLeuValAspIleIleLeuArgMetGluAspLysLysGluProVa 602
     |||
Db 6673 ---CT 6674

Qy 602 lThrHisAsnLeuThrLeuArgGly------ 619
     ||||||ThrValThrGlyLeuAlaGlyAspAr
Db 6675 GACACATCAAAATAATTTGAAACCTTTGACTTAACAGTTCATAAAAAAGCCGGATAATTCA 6734

Qy 619 gThrLysAspPhePheIleGlutIleGlyLeuLysAsnAsnLysSerGlnGluLeuSerGl 639
     ||||
Db 6735 GACG--- 6771

Qy 639 nThrValLysThrAspLysThrAsnLeuGluPhe---LysAspGlyLysAlaThr----- 656
     :::|||||:::||||||||:::
Db 6772 --------CCAGATACGGATATTGAAATTACCAAAGATGGCAAAGAAAACGGATAC 6818

Qy 657 ---IleAsnLeuLysHisGlyGlu---SerLeuThrLeuGlnIleLeuProGl 672
     |||||||
Db 6819 TTTTGTTTTGGAAAACTTAAAACCAGGGAAAATATGTTCTAACAGAAATATTCCGCCAGA 6878

Qy 672 uGlyTyrTyrSerTyrLeuValLysGluThrAsp------SerGluGlyTyrLysValVal 689
     ||||||:::
Db 6879 AGGATATCAGGGGTTAAAAGAACCAATCGAAATTAATAATTCGTGAAGATGGTTCAGTCAC 6938

Qy 689 sValAsnSerGlnGluValAlaAsnAlaThrValSer------LysThrGlyLeuIleTh 706
     :::||||||||:::
Db 6939 GATGAGTGGGAAAAAGTAGCAGATGTTTTAATTTCTGGAGAAGAATAATCAAATTAC 6998

Qy 706 rSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs 726
     ||| |||:::
Db 6999 TTTAGACGTTACG-----AACCAAGCAAAGGTTCCTTTACCGTGGCCAT 7049

Qy 726 pGlnLysIleAsnGlyTyrLeuAlaLeuIle-----ValIleAlaGlyIleSerLe 743
     |||||||:::
Db 7050 AGGACGCGTTGTGGTTTTTTACTTGATAGGATTAGTACAATTCGTGATACGGGGTGTTTATCT 7109

Qy 743 uGlyIle 745
     |||
Db 7110 CTTTATT 7116

RESULT 12
US-09-663-779-1301
; Sequence 1301, Application US/09663779
; Publication No. US20030166848A1
; GENERAL INFORMATION:

```
; APPLICANT:           Corbin, David R.
; APPLICANT:           Malvar, Thomas M.
; APPLICANT:           Shukla, Hridayabhiranjan
; TITLE OF INVENTION:  BACILLUS THURINGIENSIS CHROMOSOMAL GENOME SEQUENCES AND USE
; TITLE OF INVENTION:  THEREOF
; FILE REFERENCE:                 38-21(51376)B
; CURRENT APPLICATION NUMBER:     US/09/663,779
; CURRENT FILING DATE:            2000-09-15
; PRIOR APPLICATION NUMBER:       60/154,678
; PRIOR FILING DATE:              1999-09-17
; NUMBER OF SEQ ID NOS:           8283
; SEQ ID NO 1301
; LENGTH: 10627
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-663-779-1301

Alignment Scores:
Pred. No.:
Score:                 185.50
Percent Similarity:    38.44%
Percent Identity:      21.50%
Best Local Similarity: 4.70%
Query Match:           29

US-09-494-297-2 (1-757) x us-09-663-779-1301 (1-10627)
```

```
Db:                                         Length:       10627
                                            Matches:      132
                                            Conservative: 104
                                            Mismatches:   209
                                            Indels:       169
                                            Gaps:         32
```

```
Qy    731 GlyTyrLeuAlaleullevallleAlaGlyIleSerleuGly 744
              ||| :::           ||::|||::||:::|||
Db   5522 GGT--------AAAGTAAAAATCTCAGACTTATCTGTAGGA 5554
```

RESULT 13
US-10-417-884-864
Sequence 864, Application US/10417884

GENERAL INFORMATION:
  APPLICANT: Lynn A Doucette-Stamm and David Bush
  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                      ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

  NUMBER OF SEQUENCES: 7310

  CORRESPONDENCE ADDRESS:
    ADDRESSEE: GENOME THERAPEUTICS CORPORATION
    STREET: 100 Beaver Street
    CITY: Waltham
    STATE: Massachusetts
    COUNTRY: USA
    ZIP: 02354

  COMPUTER READABLE FORM:
    MEDIUM TYPE: CD/ROM ISO9660
    COMPUTER: PC
    OPERATING SYSTEM: <Unknown>
    SOFTWARE: ASCII

  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/417,884
    FILING DATE: 17-Apr-2003

  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/107,532A
    FILING DATE: 30-Jun-1998
    APPLICATION NUMBER: 60/085,598
    FILING DATE: 14 May 1998
    APPLICATION NUMBER: 60/051571
    FILING DATE: July 2, 1997

  ATTORNEY/AGENT INFORMATION:
    NAME: Ariniello, Pamela Deneke
    REGISTRATION NUMBER: 40,489
    REFERENCE/DOCKET NUMBER: GTC-012

  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (781)893-5007
    TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 864:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2187 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: circular
    MOLECULE TYPE: DNA (genomic)
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
    ORIGINAL SOURCE:
      ORGANISM: Enterococcus faecium
  FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 1...2187
    SEQUENCE DESCRIPTION: SEQ ID NO: 864:

US-10-417-884-864

Alignment Scores:
Pred. No.:
  Score: 182.00   Length: 2187
  Pred. No.:   4.73e-05   Matches: 155
  Percent Similarity: 34.82%   Conservative: 103
  Best Local Similarity: 20.92%   Mismatches: 238
  Query Match: 4.61%   Indels: 245
  DB: 52   Gaps: 40

```
Qy    72 TrpTyr-------------GlyTyrGluSerTyrValArgGlyHis-ProTyrTy 85
            |||||          |||: ::||||||| |||
Db   468 TGGTACACTTTCAGTCAAGAGTGTGGGGACAAGTCCTAC----AACGGTCACTCCA----- 519
```

US-09-494-297-2 (1-757) x US-10-417-884-864 (1-2187)

```
Qy    85 rLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGlyLySer------ArgSe 103
            :::::::||||||:::|||||||:::||||||||||:::         :.||
Db   520 -------------------------TCTATTTCCATAGAAGGAGAAAATACCAACAAG 551
```

```
Qy   103 rTyrTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerVa 123
            | ||||:|||                            ||||||
Db   552 CAATCAGATCTAT----------------------------------TTAGGAAAAGACCAAGAAAT 584
```

```
Qy   123 lLysLysTrpTyrLeuLysHisAspGlyIleSerThrLysPheGluAspTyr------- 140
            ||  ||||:::                    :::         |||
Db   585 CCAAATCCATTACCAAGGTCAGA--------ATCCAAACAGAAAAATGAGGACTTCCATCCAAA 638
```

```
Qy   141 --------------AlaMetSerProArgIleThrGlyAspGlu 151
                          |||  ::||||||
Db   639 TTTCTGGTGATCAAAATGAACGGCAGGACAACTTTCCAGCCAAACATTGATACCAATGAATT 698
```

```
Qy   151 uAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMe 171
            |||        ||||||  |||                       ||||||
Db   699 AGCTGAA----------AAAAAGTTATGGGAAGAATT 716
```

```
Qy   171 tGluGlyLeuGluProLeuAsnAlaIleAlaArgValThrGlnLeuGluValTrpTyrYse 191
            |||                ::: |||                    |||
Db   717 ATCTGCTAAAGCTCCCGGAGTCAGTCTTCACATC------AAAAAGTTATGGAAGAATT 770
```

```
Qy   191 rAspAsnAlaProIleSerAsnProAspGlu---SerPheLysArgGluSerGluSerAs 210
            ||||||||                    |||:|||:::            :::
Db   771 TGACAACAATCTAGCTGATCGTCCAGATCAAGTTACTTTTGAGATTCAACGGGAA----- 825
```

```
Qy   210 nLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLeuGlnLeuIleAspPr 230
            |||                :::                    :::  ||
Db   826 -----CATACGACAAATGCTGCCAGCTTGGGAAAAACGGATATATTGAATCATTAAACC 878
```

```
Qy   230 oAsnLeuAlaThr----------------LysMetProLysGlnVa 240
            |||                                  ||:::
Db   879 AGGTAAAGATACAACAAATACGTGGGAACGTGCAGACATTGACAAAATTATCTGCACATAG 938
```

```
Qy   240 lProAspAspPheGln------LeuSerIlePheGluSerGluAspLysAspLysSerTy 258
            |||                  |||:::||     |||           :::
Db   939 CGGGAGAAAAGTTATCAAGGAGATATTATCACTACCCTCAAATACACAATTCAAGCAATT 998
```

```
Qy   258 rAsnLysGlyTyrGlnAsnLeuLeuSerGlyIleGlyLeuValProThrLysProThrPr 278
            :::||||||                       |||:::
Db   999 CAGT-----TACCAAACAATC------AAAGAAATTACCTGTACC 1031
```

```
Qy   278 oGly----------AspProProMetProProAsnGlnProGlnThrThrSe 292
            |||          |||                          ||| ||| :::
Db  1032 AGGATACGGATTCTCAACAAATATGACATGGAAAAATACTAAACAATTCACACC 1091
```

```
Qy   292 rVal------LeuIleArgLysTyrAlaIleGlyAspTyrSerLysSerLeuLeuGluGl 309
            |||      |||:::                       |||||  |||
Db  1092 GTTAAACTTGAAAATAACGAAAAAAATTCCTCTACAGGTGAA-----AAGGATCTTATTGG 1145
```

```
Qy   309 yAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAla---ArgValPheSe 328
            |||                    ||||||                     |||
Db  1146 CGCTGTTTTCAAATTAACGAGGACGATTCTTATTACTTTAACAGATCATCATGGCGACGG 1205
```

```
Qy   328 rSerAsnAspIleGlyGlyValArgIleGlyLeu---SerAspGlyThrTyrThrLeuThr 347
            :::            |||                 |||:::               |||
Db  1206 AACCTATTCTCTTCCAGAAAATGTCAAAATTGCAAAAGAAATGACCTATACGGCTGACAGA 1265
```

```
Qy   347 uLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysLysValGluAlaGl 367
            |              |||:::||||||                ||||::||||
Db  1266 AACAAAAAGTCCAGAAGGGCATGGATTAAGCAAAAAGACTACTTGGGAAATCGC 1325
```

```
Qy   367 yLysValTyrThrIle---IleAspGlyLys----------- 376
            |||:::                |||||||||||
Db  1326 TTCTGAGGTACGGTAACCATTGATGAAAAAACAGTGCTACTACTTCCGATGATACGATCCA 1385
```

```
Qy   377 ----GlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGlyAlaTyrAs 395
            ||||||||||||||     |||:::               |||
Db  1386 GTTGACTATTGAAAAATCCTTTGTTGAAGTT------CCTGGAGCACTAAGGTATGC 1439
```

```
Qy   395 nAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLy 415
```

Alignment Scores:
Pred. No.:
Score: 6.84e-05
Percent Similarity: 180.00
Best Local Similarity: 34.6%
Query Match: 20.95%
                                4.56%
                                26

Length: 2127
Matches: 150
Conservative: 98
Mismatches: 270
Indels: 198
Gaps: 33

US-09-494-297-2 (1-757) x US-09-600-720-17 (1-2127)

```
Qy  1440 GATGCAAGGAGGACGGACAAAAGAGATAAAATCTTAAAGGAGGACAGCCATTTTCCCTACAGAAAAA 1499
              |||    :::                                            |||
Db  2151 G                                                                  2151

Qy   415 sAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPr 435
             ||||||||                      ::: |||  :::
Db  1500 AGAAGCAAATGGTTACTTATCAG                    CCAAT            1526

Qy   435 oAspSerGlu----------AspGlyGlyLysThrMetThrProAspPheThrThrGlyGl 452
             ||||||:::         |||                   |||  |||::
Db  1527 TGACACGCCAAACAACGAATGAAAAAGGTCTTCCCAGTTTGAATTCACTCACACCTGGTAA 1586

Qy   452 uValLysThrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAs 472
             |||||||                  :::
Db  1587 ATATCGAGTCGTTGAAACAGCTGGTCCTGCCGGATAT                        1625

Qy   472 pThrAspProAspThrPheLeuLysHisIleLeuLysLysValIleGluGlyTyrArgGl 492
             |||               |||::                |||::
Db  1626 TACTTCCGCCGGGAAATTATGAATTCCAAATCGATAAAATAT                   1665

Qy   492 uLysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgAlaAlaThrGl 512
             |||                |||||     ||||::|||
Db  1666 ---GGAAAAAATCATT----TACACGGGAAAAAATACCGAGAGTGAAGTGTATGGAC 1718

Qy   512 nLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLysLeuLysAspTy 532
             |||                   |||  ::: |||      ::: |||
Db  1719 GCTCACTCATCAAAATCGACTAAAAGGCTTTGATCTAACGGTACACAAAAAGAAGAC--      1776

Qy   532 rHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTy 552
             |||          |||    :::|||
Db  1777 ---AACGGACAGACATTTAAAAAGAGACAAAAATTCAGACTGCAG--                1815

Qy   552 rAlaGlnAspSerAsnProProGlnLeuThrAspSerPhePheIleProAsnAsnAsn 572
             |||||::           ||||||:::
Db  1816 GGACCAGAAATG--  GACTTAGAA                                      1836

Qy   572 nLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIleAr 592
             |||                   |||::|||
Db  1837 TCGCCAAAAGAT--                                                 1848

Qy   592 gMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrVa 612
             |||||      |||       |||||
Db  1848 AACGGACAGACATTTAAAAAGAGACAAAAATTCAGACTGCAG--                  1815

Qy   612 lThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluGluLeuLysAsnAs 632
             |||      |||          |||||||
Db  1849 GGACAAGAAACAGAATACCTTTCTATTCGAA                               1878

Qy   632 nLysGlnGluLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAs 652
             |||                   |||||
Db  1878                                                                1878

Qy   652 pGlyLysAlaThrIleAsnLeuLysHisGlyGlu----SerLeuThrLeuGlnGlyLeuPr 671
             |||||                  |||    :::
Db  1879 AATTTAAAACCTGGACTTATACGCTCACCGAAACTTTTACACC                   1922

Qy   671 oGluGlyTyrSerTyrLeu------ValLysGluThrAspSerGlnGlyTyrLysVa 688
             ||||||||||                   |||
Db  1923 AGAAGGAATACCAAGGTCTCTAAAAGAGCCAGTTACTATAGTTATACAGAAGATGGGTCAAT 1982

Qy   688 lLysValAsnSerGlnLeuValAlaLeuAsnAlaThrValSerLysThrGlyIleThrHisSerAs 708
             :::          |||                 :::|||
Db  1983 TCAAGTGGATGGAACAAGAT--  CATGAATCTGTTCTGTCACCAGAGCCAAAAACAA     2036

Qy   708 pGlu----ThrLeuAlaPheGluAsnAsn----LysGluProValValProThrGlyValAs 726
             :::                     |||    ::: |||
Db  2037 CCAGATTTCTTTTAGACATCACCAAAAGTACCATTACCTGAAACGGGAGAGAAT         2096

Qy   726 pGlnLysIleAsnGlyTyrLeuAlaLeuIleVaIleAlaGlyIleSerLeuGlyIleTr 746
             |||                   |||::  :::    |||||
Db  2097 TGGCCGTTTAGGAAATCTAT----                                       2150
```

Qy 746 p 746
         |
Db 746

```
US-09-494-297-2 (1-757) x US-09-600-720-17 (1-2127)

Db  2151 G 2151

Qy    68 SerGluTyrArgTrpTyrGlyTyrGluSerTyrValArg---GlyHisProTyrTyrLys 86
             :::|||||||||||||||||:::                |||||||||:::
Db   201 GCAGAGCAGCTTTATTATGGGGTGGAATGAGAACGGAGCAGACAAAGTTCGCCATAATTTT--- 257

Qy    87 GlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyrGlnVal 106
             |||  :::        |||
Db   258 --TTGTACCTATCCCTAAAAATCCTCCAAAGCCTGAATTAAAAGACGAGTATGTTGTT 314

Qy   107 TyrCysPheAsnLeuLysSerAlaPheProLeuGlySerAspSerSerValLysLysTrp 126
             |||||||||||||||||       ::: |||                    :::
Db   315 TATTGCTTTAACAAAAAATTGTATTGGGCAGATCAAATGGGAAATCTTATATACAGCAAATTTT 374

Qy   127 T-----------------------------TyrLysLysHisAspGlyTyrLeuSer 134
             |||                                 |||::|||
Db   375 AATGACATCAGATCTCCAATAAAGGATTTACCTGTATATGAGAAAACTAGGATATGAT 434

Qy   135 ThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLys 154
             ||||||:::        |||                    :::
Db   435 GGTATATTTAAACAAAATATGCTCCAGATTACAAAAAAGATAATTAGTGAAGTGCCT 494

Qy   155 LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlyGly--- 173
             |||  ::: |||                 :::
Db   495 TTGGTGGCAGTTTAAGTAATGAATGGGATACCCCACTAACAAGTCACACTACAACTAGGCTAC 554

Qy   174 ---LeuGluProLeuAsnAlaIleArgValThrGlnLeuAlaValAlaValTrpTyrTyrSerAsp 192
             |||                  :::|||||||:::
Db   555 CATTTAAAATAATGATTTCTTCTAGAAAAAAGTTACTCAATTACCATTGGTATTTTAGTGTGAT 614

Qy   193 AsnAlaProIleSerAsnProAspSerPheLysArgGluSerGluAsnLeuVal 212
             |||                  ::: |||
Db   615 ---------AGTTTACAAAAGAATAACCTTAAAGATACGGGTGGTTATAACTTA--- 659

Qy   213 SerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleLeuAspProAsnLeu 232
             :::|||                  ||||||:::
Db   660 ------------AACGATATTGGAAAAAAAGCTTTAGATTTTTTAATCACTGAGAGAG 707

Qy   233 AlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGlu 252
             :::||||||:::                 |||
Db   708 GATTCTAACCTT----AAATCAGACGAGAGTAATTACTCAATTGGATAATTTTTATCAA 764

Qy   253 AspLysGlyAspLysTyrArgAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValPro 272
Db   708 ...
```

Db 765 AGTGGCGGGCATGACCATATGAAAGATTACCAAAAATCTTCGGCCTCTACCTTAATTCCT 824
         ::: ||||||||||||| ||||::::|||
Qy 273 ThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSer 292

Qy 825 AAAGAACCGCTAAAGCCT 842
              |||:||||
Db 293 ValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeu 312

Db 843 ---------------------CAGCTAGGTGGTTTTAGT---- 860
                              :::||||||
Qy 313 GlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerAsnAspIle 332

Qy 861 --GGACAATTGAAATGGAATGGATTAAGCGGCCTTGAAGGAGGATCATCAGGTTCA 911
             |||| ||||||||
Db 333 GlyGluArgIleGluLeuGluAspGlyThrThrTyrThrLeuThrGluAsnSerProAla 352

Db 912 CAAGAAAACTAATAGAA----- 959
              ||||| |:|
Qy 353 GlyTyrSerIleAlaGlu----------ProIleThr----PheLysValGluAlaGly 367

Qy 960 GGACTCTTCAGGAACGGGAGGGCAAAACGAGAGATCCTTTGCCAGGATTGAAGGGTGGT 1019
                ||| ||||||||||| ||||||||||||
Db 368 LysValThrTyrThrIleIleLeuAspGlyLysLysGlnIleIleGluValGluValGlu 387

Db 1020 GCACCTGATACA------ 1055
              :::   :::
Qy 388 ProTyrSerValGlyLeuAlaThrTyrAsnAspPheGluGluPheSerValLeuThrThrGlnAsn 407

Qy 1056 --CAAGGTCTTGAAGGGGTAAC---------- 1097
                 ||| |||| |||||||
Db 408 TyrAlaLysPheTyrTyrAlaLysLysAsnGlySerGlnValValTyrCysPhe 427

Db 1098 TATGGTTAGT---------- 1142
              ::: |||
Qy 428 AsnAlaAlaSerProLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrProAsp 447

Qy 1143 GAAACCGAAGATACTAACCCACCTGGTATACTACTAGGCGGCCTCAGGAAAATGTCGAA-- 1199
         ||||||||||||
Db 448 PheThrThrGlyGluValLysTyrThrHisIleAlaGly---------------- 461

Db 1200 ---ACGCATGAAAGATACTAGAAACCCTCAtCTGAtGGGGAtCGGGGCGGGTCTAGCTGGC 1256
            ::: |||
Qy 462 AspLeuPheLysTyrThrValLysProArg---------------- 472

Qy 1257 GAATCAGGAGGAAAACGACACCTAAACACCAGGACAAACCGCGGGGGAACCAGTCATCGAG 1316
              ::: |||
Db 473 ThrAspProAspThrPheLeuLysHisIleIleLysGluGlyTyrArgGlu-- 492

Db 1317 ACAACAGAGGATACA---------- 1334
              |||:
Qy 493 LysGlyGlnAlaIleGluLysTyrSerGlyLeuThrHisGlnThrLysValAlaAlaAlaThrGln 512

Qy 1335 AAAGGCATGTCTGGACAAATCTGGTGGCCATATCGAGTCAGAAAACACCAGGACGGGAGTC 1394
              ::: |||
Db 513 LeuAlaIleLeuTyrTyrPheThrAspSerAlaGluLeuAspPheIleProAsnAsnAsn 532

Db 1395 GTCATGATTGGTCGTTCAGGGACAAACCATCGAGACAACAGAGGACACAAAAA---- 1448
              ::: |||
Qy 533 HisGlyPheGlyLysMetAsnAspSerThrLeuuAlaValAlaAlaLysIleLeuValGluTyr 552

Qy 1449 --GGCCATGTCTGGACAAAATCTGGCCGTACTATCCGAG---- 1481
              ::|||||
Db 553 AlaGlnAspSerAsnProProGlnIleLeuThrAspLeuAspPhePheIleProAsnAsnAsn 572

Db 1482 TCAGAGGAGACACTAAGAAAACCTGAGGTC---------- 1508
              ::||||:||:||
Qy 573 LysTyrTyrGlnSerLeuIleGlyThrGlnThrTrpHisProGluAspLeuValAspIleIleArg 592

Qy 1509 --------ATGATTGGTGGGTCAG---------- 1523
              ::||||||||||| |||
Db 593 MetGluAspProLysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrVal 612

Db 1524 ----------GGACAAAATCATCGACTTCTCTGAAAAC----ACCCAATCAGGTGTATG 1565
              |||||||||||
Qy 613 ThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLeuAsnAsn 632

Qy 1566 TCTGGGGCAGTCTTGGTGACACTACG---------- 1598
              :::||| |||| GTAATTGAG
Db 633 LysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuProPheLysAsp 652

Db 1599 ------------GATCCAAGAAGAGTCTGAGATAATCATTGGTGGG 1631
              ::: |||
Qy 653 GlyLysLysAlaThrThrIleAsnLeuLeuLysHisGlyGluSerLeuThrLeuGlnGlyLeuProGlu 672

Qy 1632 CAAGGACAAAATCATCGACTTCTCTGAGGATACTACGCGGGGTATGTCTGGT---CAATCT 1688
              :::|||
Db 673 GlyTyrSerTyrLeuValLysGluThrGlyGlyTyrLysValLysValAsnSer 692

Db 1689 GGAGGCAGTACAATTGTCGAAGACACCAAGAGAGCCGAGACCTAAGCCTAAAACCTGACCT 1748
              :::|||
Qy 693 GlnGluValAlaIleAsnAlaThrValSerLysThrGlyIleIleThrHisSerAspGlyThrLeuuAla 712

Qy 1749 GCGCCCAATTGTTAAT---------- 1769
              :::||| GACGAA
Db 713 PheGluAsnAsnLysGluProThrGlyValAlaProThrGlyGlyValAlaAspGlnLys-- 728

Db 1770 --AAACCTAACAAAAGCCACTCATCTCCCACAGACAAGTGATATGAAGCAACTCACCCTA 1826
              :::|||
Qy 729 ---IleAsnGlyTyrLeuuAlaLeuIleValAlaIleAlaGlyIleSerLeu 743

Qy 1827 AGCATCATCGGTGCAAATGTCAAATGCTCGTTGTCCTATGTCTGTCTCTA 1874
              :::|||
Db   (end)

RESULT 15
US-10-269-017-17

; Sequence 17, Application US/10269017
; GENERAL INFORMATION:
; APPLICANT: GUSS, Bengt et al.
; TITLE OF INVENTION: NOVEL FIBRONECTIN-BINDING PROTEIN
; FILE REFERENCE: 0825-0172P
; CURRENT APPLICATION NUMBER: US/10/269,017
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Streptococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(1901)
US-10-269-017-17

Alignment Scores:
Pred. No.:
Score: 6.84e-05
Score: 180.00
Percent Similarity: 34.64%
Percent Identity: 20.95%
Best Local Similarity: 4.56%
Query Match: 49

Length: 2127
Matches: 150
Conservative: 98
Mismatches: 270
Indels: 198
Gaps: 33

US-09-494-297-2 (1-757) x US-10-269-017-17 (1-2127)
DB:

Qy   68 SerGluTyrArgTrpTyrGlyTyrGluSerTyrValArg--GlyHisProTyrTyrLys 86
             :::|||
Db   201 GCAGAGCAGCTTTATTATTATGGGTGGAATGATGGAACGAGACAAAAGTTCGCCATATTTT--- 257

Qy   87 GlnPheArgValAlaHisSerAspLeuArgValAsnLeuGluGlySerArgTyrArgGlnVal 106
             ||::|||
Db   258 --TTGTACGTATCGCCTAAAAAATGTTCCAAAGCGTGAATTAAACACGAGTATGTTGTT 314

Qy   107 TyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLysTrp 126
             |||||||||||
Db   315 TATTGCTTTAACAAAAAAAATTGTTATTGGCCCAGATCAATGGGAATCTAATACAGACAATTT 374

Qy   127 ---------- ------------------------ TyrLysLysHisAspGlyIleSer 134
             :::
Db   (end)

```
Db   375  AATGACATCAGATCTCCATATAAACGATTTACTGTATATGAGAAAAAACTAGGATGATGAT  434
               |||::::|||

Qy   135  ThrLysPheGluAspThrTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLys  154
               ::::||||         :::|||||                |||
Db   435  GGTATATTTAAACAATATGCTCCAGATTACAAAAAAGATATTAGTGATATTCCAAGTGCT  494

Qy   155  LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly---  173
               |||||||||      |||:::        |||   :::
Db   495  TTGGTGGCAGTTTTAAGTAATGGATAACCCACTAACAAGTCACTACTATCAACTAGCTAC  554

Qy   174  ---LeuGluProLeuAsnAlaIleLeuArgValThrGlnIleAlaLeuValTrpTyrTyrSerAsp  192
               |||             ::::|||        ||||||::::||||||
Db   555  CATTTAAATAATGATTCTTCTAGAAAAAGTTACTCAATTGCATTTGGTTATTTAGTGAT  614

Qy   193  AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGluSerAsnLeuVal  212
               |||            |||         |||:::
Db   615  ---------AGTTTAACAAAAGAATACCTTAAACATACCGGTGGTTATAACTTA---  659

Qy   213  SerThrSerGlnLeuSerLeuMetArgGlnAsnAlaLeuLeuLysGlnLeuLeuAspProAsnLeu  232
               :::::||||||||||          |||||||
Db   660  -----------AACGATATCGGAAAAAAAAGCTTTAGATTGTTTTTAAATCAGTAAAGAGAG  707

Qy   233  AlaThrLysMetProLysGlnIleValProGluAspPheGlnLeuLeuSerIlePheGluSerGlu  252
               ::::||||||           :::|||||||||::::
Db   708  GAATTCTAAGCTTT---AAATCAGCAGCAGAGTAATTACTCCATTGGATATTTATGTTTATCAA  764

Qy   253  AspLysGlyAspLysTyrAsnLysGlyIleTyrGlnAsnLeuLeuSerGlyGlyLeuValPro  272
               |||        |||         |||||||
Db   765  AGTGGCGGGCATGACCATATGAAAAGAATTACCAAAAATCTTCTCGGCTCTACCTTAATTCCT  824

Qy   273  ThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSer  292
               :::::||||||
Db   825  AAAGAACCGCTAAAGCCT  842

Qy   293  ValLeuIleArgGlyTyrAlaIleGlyAspTyrSerLysLeuLeuLeuGlyAlaThrLeu  312
               :::::||||||         ::::|||
Db   843  ---------------CAGCTAGGTGGTTTAGT---  860

Qy   313  GlnLeuThrGlyAspAsnValAsnSerPheGlnLnAlaArgGlyValPheSerSerAsnAspIle  332
               ------|||||||||                :::|||
Db   861  ------------GGACATAATGGAAAATGATTAAGCGGCCTTGAAGGAGGATCATCAGGTTCA  911

Qy   333  GlyGluArgGlyIleGluLeuSerAspGlyThrThrThrThrLeuThrGlnLeuAsnSerProAla  352
               |||||                   :::|||
Db   912  CAAGAAAACTAATGAA------GATGGTAAGAAAAGGACTT------ATAGGTTCCATGGA  959

Qy   353  GlyTyrSerIleAlaGlu---  367
               |||:::||||         :::||||||
Db   960  GGACTCTCAGGAAGCGGAAACGAGATCCTTTGCCAGGATTGAAGGGTGAGGTGGT  1019

Qy   368  LysValThrTyrThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGluValGlu  387
               |||          ::::|||
Db   1020 GCACCTGATACA------CCTCAAAAGCCTAATGATCCATTG---  1055

Qy   388  ProTyrSerValGluAlaTyrAsnAspPheGluPheSerValLeuThrThrGlnAsn  407
               ::::|||          |||||
Db   1056 ---CAAGGTCTTGAAGGCGGTAAC------TCTCCTATAGTAGAGAACAAAAC  1097

Qy   408  TyrAlaLysPheTyrTyrAlaLysSerGlnValValTyrCysPhe  427
               |||          ::::
Db   1098 TATGGTAGT------ACCGAAGGATATCATGGTCAATCAGGCATTCTTGAG  1142

Qy   428  AsnAlaAspLeuLysSerProProAspGluGlyLysGlyLysThrMetThrProAsp  447
               |||||                :::|||
Db   1143 GAAACCGAAGATACTAACCCACCTGTATCAATACTAGGCGGCTCAGGAAAATGTCGAA---  1199

Qy   448  PheThrThrArgGlyLeuValLeuSerTyrThrHisIleAlaGly---  461
               |||       :::|||
Db   1200 ---ACCGATGAAGATACTAGAAACCCTCATCTGATCGGGATCGGCGGGGTCTAGCTGGC  1256

Qy   462  AspLeuPheLysTyrThrValLysProArg---  472
               :::
Db       ---Asp  472
```

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Db   1257  GAATCAGGAGGAAACGACACCTAAACCAGGACAAACCGGCGGGGAAGGAGGACCAGTCATCGAG  1316

Qy   473   ThrAspProAspThrThrPheLeuLysHisIleIleGluLysLysValIleGluGluGlyTyrArgGluGlu  492
                ||||||                  |||:::
Db   1317  ACAGACAGAGGATACA------CAA  1334

Qy   493   LysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnIleLeuArgGlnAlaAlaThrGln  512
                |||             :::
Db   1335  AAAGGACATGTCTGGACAATCTGGTGCACTATCGAGAAAAACACCGGAG  1394

Qy   513   LeuAlaIleTyrTyrPheThrAspSerArgAlaGluLeuAspLysSerLeuLysAspTyr  532
                |||                ::::|||
Db   1395  GTCATGATTGGTGGTCAGGACAAAACCATACGAGACACCAACAGGAACACA-----  1448

Qy   533   HisGlyPheGlyAspMetAsnAspProSerThrLeuAlaValAlaLysIleIleLeuValGluTyr  552
                |||          ::::
Db   1449  ---GGCATGTCTGGACAATCTGGGCGGTTACTAATATCGAG  1481

Qy   553   AlaGlyGlnAsnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsn  572
                |||::::||||
Db   1482  TCAGAGGACACTAAGAAAACCTGAGGTC---  1508

Qy   573   LysTyrTyrGlnSerLeuIleGluGlyThrGlnThrProHisProGluAspLeuValAspIleIleArg  592
                :::::||||||         :::
Db   1509  --ATTGATTGGTGGTCAG  1523

Qy   593   MetGluAspLysLysGlyValIleLeuProValThrHisAsnLeuThrLeuArgLysThrArgVal  612
                |||       |||:::          :::
Db   1524  ---GGACAAAATCATCGACTTCTCTGAAAAC-----ACCCAATACAGGTATG  1565

Qy   613   ThrGlyLeuAlaGlyAspGlyAsnProArgThrLysAspProPheHisGluIleGluLeuLysAsnAsn  632
                |||||||            ::::
Db   1566  TCTGGGCAGTCTGGTGACACTACG------GTAATTGAG  1598

Qy   633   LysGlnGluGluLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAsp  652
                ::::||||||         |||:::
Db   1599  --------------GATACCAAGAAGTCTGAGATAATCATTGGTGGG  1631

Qy   653   GlyLysAlaThrIleLeuAsnLeuLysHisGlyIleGluSerLeuThrLeuGlnGlyLeuProGlu  672
                |||::::||||                :::|||
Db   1632  CAAGGACACTACAAATTGTCGAAGACACCAGAAGCCTAGCCTTAAACCTGCACCT--CAAATCT  1688

Qy   673   GlyTyrSerTyrLeuValLysGluThrArgSerGluGlyTyrArgLysValLysValAsnSer  692
                |||||                   :::|||
Db   1689  GGAGGCACTACAAATTGTCGAAGACACCAGAAGCCTAGCCTTAAACCCTGCACCT  1748

Qy   693   GlnGluValAlaAsnAlaThrValSerLysTyrIleGluThrSerAspGluThrLeuAla  712
                |||::::||||||         :::
Db   1749  GCGCCAATTGTTAAT------GACGAA---  1769

Qy   713   PheGluAsnAsnLysGluProValValProThrGlyValAspGlnLys------  728
                :::|||             |||
Db   1770  ---AAACCTAACAAAGGCACTCATCCCACAGACAAGTGATATGAAGAAACTCACCCTA  1826

Qy   729   ---IleAsnGlyTyrLeuAlaLeuLeuValIleIleAlaGlyIleSerLeu  743
                |||            ::::||||
Db   1827  AGCATCATCGGTGCAATGTCAAATCCTGCTTGTCCTATGTCTGTGTCTCTA  1874
```